



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori
- (ii) TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DLA PIPER RUDNICK GRAY CARY
 - (B) STREET: 1650 Market Street, Suite 4900
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19103-7300
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/808,031
 - (B) FILING DATE: 03-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: T. Daniel Christenbury
 - (B) REGISTRATION NUMBER: 31,750
 - (C) REFERENCE/DOCKET NUMBER: 1033-CIP3-CON-03
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-656-3381
 - (B) TELEFAX: 215-656-2498

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 640..2094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG	60
TGTACCGCGT TTCCCTGGAT GGTCACCTGG TGGCGGTGGA GTGGGGCCCCG CGCACGGGCT	120
CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG	180
CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCCTCGGCA TTGGTCTAAA	240
CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG	300
ACGACGTGCG CTTACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGATCA GCCTGAGCGC	360
CTCGAGCGGC GGAGCGGCGT TCGCGCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG	420
TAGCCTGTTC TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGGTA GCGGAGCCAA	480
CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG	540
CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT	600
GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG	654
Met Thr Ala Arg Leu	
1 5	
GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG	702
Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu	
10 15 20	
CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG	750
Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg Glu Ala Arg Arg	
25 30 35	
CTC GCG CAC GAA GCG TTG CTC GTC CCG GCG AAG GCC ATC GAC GAA GCG	798
Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala	
40 45 50	
GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC	846
Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu	
55 60 65	
GCG GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG	894
Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys	
70 75 80 85	
GCC TGG AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGC CGC GCG CTG	942
Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu	
90 95 100	
AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG	990
Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu	
105 110 115	

GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC	1038
Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp	
120 125 130	
GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG	1086
Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu	
135 140 145	
GAC TCC GCG GAG GCG CTG GCC AAG GCG CTG GGG CTG AGC GTC TCC AAG	1134
Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly Leu Ser Val Ser Lys	
150 155 160 165	
CTC CGC TGG TTC GCG TTC CAC CGG GAG GTC GAC ACG GCC ACG CAC TAC	1182
Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr	
170 175 180	
GTG AGC TGG ACC ATT CCG AAG CGG GAC GGC AGC AAG CGC ACG ATT ACG	1230
Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr	
185 190 195	
TCC CCC AAG CCT GAG CTG AAG GCA GCG CAG CGC TGG GTG CTG TCC AAC	1278
Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn	
200 205 210	
GTC GTG GAG CGG CTG CCG GTC CAC GGC GCC GCC CAC GGC TTC GTG GCG	1326
Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala	
215 220 225	
GGA CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTC	1374
Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val	
230 235 240 245	
GTG GTC AAG GTG GAC CTC AAG GAC TTC TTC CCC TCC GTC ACC TGG CGC	1422
Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg	
250 255 260	
CGG GTG AAG GGC CTG TTG CGC AAG GGC GGC CTG CGG GAG GGC ACG TCC	1470
Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser	
265 270 275	
ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CGG GAG GCG GTC CAG	1518
Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln	
280 285 290	
TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC	1566
Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro	
295 300 305	
CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG	1614
Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys	
310 315 320 325	
CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC	1662
Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr	
330 335 340	

ACG CGC TAC GCG GAC GAC CTG ACC TTC TCC TGG ACG AAG GCG AAG CAG	1710
Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln	
345 350 355	
CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT	1758
Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser	
360 365 370	
CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC	1806
Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp	
375 380 385	
AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC	1854
Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu	
390 395 400 405	
GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC	1902
Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg	
410 415 420	
GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC	1950
Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly	
425 430 435	
AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC	1998
Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala	
440 445 450	
GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT	2046
Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala	
455 460 465	
CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG	2094
Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu	
470 475 480 485	
TGACGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCCG CATTCAGCAA	2154
CTCCGTCAGC CGGCGCGGGT AC	2176

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ala Arg Leu Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala
1 5 10 15
Val Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys
20 25 30

Arg Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys
 35 40 45
 Ala Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu
 50 55 60
 Val Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser
 65 70 75 80
 Glu Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr
 85 90 95
 Glu Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr
 100 105 110
 His Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
 115 120 125
 Ala Asp Ala Phe Asp Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn
 130 135 140
 Gly Leu Thr Glu Leu Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly
 145 150 155 160
 Leu Ser Val Ser Lys Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp
 165 170 175
 Thr Ala Thr His Tyr Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser
 180 185 190
 Lys Arg Thr Ile Thr Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg
 195 200 205
 Trp Val Leu Ser Asn Val Val Glu Arg Leu Pro Val His Gly Ala Ala
 210 215 220
 His Gly Phe Val Ala Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His
 225 230 235 240
 Gln Gly Ala Asp Val Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro
 245 250 255
 Ser Val Thr Trp Arg Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu
 260 265 270
 Arg Glu Gly Thr Ser Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro
 275 280 285
 Arg Glu Ala Val Gln Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly
 290 295 300
 Pro Arg Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn
 305 310 315 320
 Ala Leu Cys Leu Lys Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg
 325 330 335

Leu Gly Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp
 340 345 350
 Thr Lys Ala Lys Gln Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val
 355 360 365
 Ala Val Leu Leu Ser Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe
 370 375 380
 Arg Val His Pro Asp Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln
 385 390 395 400
 Arg Val Thr Gly Leu Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala
 405 410 415
 Ala Arg Val Pro Arg Asp Val Val Arg Gln Leu Arg Ala Ala Ile His
 420 425 430
 Asn Arg Lys Lys Gly Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln
 435 440 445
 Leu Lys Gly Met Ala Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly
 450 455 460
 Arg Ala Phe Leu Ala Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala
 465 470 475 480
 Ala Pro Gln Ala Glu
 485

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
 1 5 10 15
 Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
 20 25 30
 Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
 35 40 45
 Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys
 50 55 60

Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	65	70	75	80
Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	85	90	95	
Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	100	105	110	
Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	115	120	125	
Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	130	135	140	
Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	145	150	155	160
Pro	Phe	Lys	Lys	Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	165	170	175	
Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	180	185	190	
Ile	Glu	Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Leu	Thr	Thr	Pro	195	200	205	
Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	210	215	220	
Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	225	230	235	240
Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	245	250	255	
Trp	Ala	Ser	Gln	Ile	Tyr	Pro	260												

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg	Pro	Trp	Ala	Arg	Thr	Pro	Pro	Lys	Ala	Pro	Arg	Asn	Gln	Pro	Val	1	5	10	15
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Pro	Phe	Lys	Pro	Glu	Arg	Leu	Gln	Ala	Leu	Gln	His	Leu	Val	Arg	Lys	20	25	30	
Ala	Leu	Glu	Ala	Gly	His	Ile	Glu	Pro	Tyr	Thr	Gly	Pro	Gly	Asn	Asn	35	40	45	
Pro	Val	Phe	Pro	Val	Lys	Lys	Ala	Asn	Gly	Thr	Trp	Arg	Phe	Ile	His	50	55	60	
Asp	Leu	Arg	Ala	Thr	Asn	Ser	Leu	Thr	Ile	Asp	Leu	Ser	Ser	Ser	Ser	65	70	75	80
Pro	Gly	Pro	Pro	Asp	Leu	Ser	Ser	Leu	Pro	Thr	Thr	Leu	Ala	His	Leu	85	90	95	
Gln	Thr	Ile	Asp	Leu	Arg	Asp	Ala	Phe	Phe	Gln	Ile	Pro	Leu	Pro	Lys	100	105	110	
Gln	Phe	Gln	Pro	Tyr	Phe	Ala	Phe	Thr	Val	Pro	Gln	Gln	Cys	Asn	Tyr	115	120	125	
Gly	Pro	Gly	Thr	Arg	Tyr	Ala	Trp	Lys	Val	Leu	Pro	Gln	Gly	Phe	Lys	130	135	140	
Asn	Ser	Pro	Thr	Leu	Phe	Glu	Met	Gln	Leu	Ala	His	Ile	Leu	Gln	Pro	145	150	155	160
Ile	Arg	Gln	Ala	Phe	Pro	Gln	Cys	Thr	Ile	Leu	Gln	Tyr	Met	Asp	Asp	165	170	175	
Ile	Leu	Leu	Ala	Ser	Pro	Ser	His	Glu	Asp	Leu	Leu	Leu	Leu	Ser	Glu	180	185	190	
Ala	Thr	Met	Ala	Ser	Leu	Ile	Ser	His	Gly	Leu	Pro	Val	Ser	Glu	Asn	195	200	205	
Lys	Thr	Gln	Gln	Thr	Pro	Gly	Thr	Ile	Lys	Phe	Leu	Gly	Gln	Ile	Ile	210	215	220	
Ser	Pro	Asn	His	Leu	Thr	Tyr	Asp	Ala	Val	Pro	Thr	Val	Pro	Ile	Arg	225	230	235	240
Ser	Arg	Trp	Ala	Leu	Pro	Glu	Leu	Gln	Ala	Leu	Leu	Gly	Glu	Ile	Gln	245	250	255	
Trp	Val	Ser	Lys	Gly	Thr	Pro										260			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Val	Leu	Tyr	Arg	Ile	Gly	Ser	Asp	Asn	Gln	Tyr	Thr	Gln	Phe	Thr	1	5	10	15
Ile	Pro	Lys	Lys	Gly	Lys	Gly	Val	Arg	Thr	Ile	Ser	Ala	Pro	Thr	Asp	20	25	30	
Arg	Leu	Lys	Asp	Ile	Gln	Arg	Arg	Ile	Cys	Asp	Leu	Leu	Ser	Asp	Cys	35	40	45	
Arg	Asp	Glu	Ile	Phe	Ala	Ile	Arg	Lys	Ile	Ser	Asn	Asn	Tyr	Ser	Phe	50	55	60	
Gly	Phe	Glu	Arg	Gly	Lys	Ser	Ile	Ile	Leu	Asn	Ala	Tyr	Lys	His	Arg	65	70	75	80
Gly	Lys	Gln	Ile	Ile	Leu	Asn	Ile	Asp	Leu	Lys	Asp	Phe	Phe	Glu	Ser	85	90	95	
Phe	Asn	Phe	Gly	Arg	Val	Arg	Gly	Tyr	Phe	Leu	Ser	Asn	Gln	Asp	Phe	100	105	110	
Leu	Leu	Asn	Pro	Val	Val	Ala	Thr	Thr	Leu	Ala	Lys	Ala	Ala	Cys	Tyr	115	120	125	
Asn	Gly	Thr	Leu	Pro	Gln	Gly	Ser	Pro	Cys	Ser	Pro	Ile	Ile	Ser	Asn	130	135	140	
Leu	Ile	Cys	Asn	Ile	Met	Asp	Met	Arg	Leu	Ala	Lys	Leu	Ala	Lys	Lys	145	150	155	160
Tyr	Gly	Cys	Thr	Tyr	Ser	Arg	Tyr	Ala	Asp	Asp	Ile	Thr	Ile	Ser	Thr	165	170	175	
Asn	Lys	Asn	Thr	Phe	Pro	Leu	Glu	Met	Ala	Thr	Val	Gln	Pro	Glu	Gly	180	185	190	
Val	Val	Leu	Gly	Lys	Val	Leu	Val	Lys	Glu	Ile	Glu	Asn	Ser	Gly	Phe	195	200	205	
Glu	Ile	Asn	Asp	Ser	Lys	Thr	Arg	Leu	Thr	Tyr	Lys	Thr	Ser	Arg	Gln	210	215	220	
Glu	Val	Thr	Gly	Leu	Thr	Val	Asn	Arg	Ile	Val	Asn	Ile	Asp	Arg	Cys	225	230	235	240
Tyr	Tyr	Lys	Lys	Thr	Arg	Ala	Leu	Ala	His	Ala	Leu	Tyr	Arg	Thr	Gly	245	250	255	
Glu	Tyr	Lys																	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val Ser Trp Thr
1           5           10           15
Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser Pro Lys Pro
20           25           30
Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val Val Glu Arg
35           40           45
Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly Arg Ser Ile
50           55           60
Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val Val Lys Val
65           70           75           80
Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg Arg Val Lys Gly
85           90           95
Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser Thr Leu Leu Ser
100          105          110
Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln Phe Arg Gly Lys
115          120          125
Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro
130          135          140
Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg
145          150          155          160
Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala
165          170          175
Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg
180          185          190
Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser Arg Val Gln Glu
195          200          205
Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp Lys Thr Arg Val
210          215          220

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Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu Val Val Asn Ala
 225 230 235 240

Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg
 245 250 255

Gln Leu Arg Ala Ala Ile His Asn Arg Lys
 260 265

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg
 1 5 10 15

Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala
 20 25 30

Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val
 35 40 45

Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu
 50 55 60

Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu
 65 70 75 80

Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His
 85 90 95

Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Pro Asp Pro Asp Met Thr Arg Val Thr Asn Ser Pro Ser Leu Gln Ala
1          5          10          15
His Leu Gln Ala Leu Tyr Leu Val Gln His Glu Val Trp Arg Pro Leu
20          25          30
Ala Ala Ala Tyr Gln Glu Gln Leu Asp Arg Pro Val Val Pro His Pro
35          40          45
Tyr Arg Val Gly Asp Thr Val Trp Val Arg Arg His Gln Thr Lys Asn
50          55          60
Leu Glu Pro Arg Trp Lys Gly Pro Tyr Thr Val Leu Leu Thr Thr Pro
65          70          75          80
Thr Ala Leu Lys Val Asp Gly Ile Ala Ala Trp Ile His Ala Ala His
85          90          95
Val Lys Ala Ala Asp Pro Gly Gly Gly Pro Ser Ser Arg Leu
100          105          110

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg Gln
1          5          10          15
Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly Lys Pro Gly Arg Glu
20          25          30
Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala Ala Phe Ile His Met
35          40          45
Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala Gln Leu Thr Glu Leu
50          55          60
Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu
65          70          75

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Gly Lys Glu Gly His Ser Ala Arg Gln Cys Arg Ala Pro Arg Arg Gln
1           5           10           15

Gly Cys Trp Lys Cys Gly Lys Pro Gly His Ile Met Thr Asn Cys Pro
20           25           30

Asp Arg Gln Ala Gly Phe Leu Gly Leu Gly Pro Trp Gly Lys Lys Pro
35           40           45

Arg Asn Phe Pro Val Ala Gln Val Pro Gln Gly Leu Thr Pro Thr Ala
50           55           60

Pro Pro
65

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr
1           5           10           15

Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys
20           25           30

Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser
35           40           45

Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro
50           55           60

Val Ala Val Leu
65

```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser
1           5           10           15
Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys
          20           25           30
Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser
          35           40           45
Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu
          50           55           60
Gly Val Val Leu
          65

```

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Tyr Lys Asn Leu Leu Pro Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala
1           5           10           15
Asn Leu Ile Cys Ser Lys Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly
          20           25           30
Ser Arg Gly Leu Ile Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser
          35           40           45
Ala Gln Ser Met Lys Lys Val Val Lys Ala Arg Asp Phe Leu Phe Ser
          50           55           60

```

Ile Ile Pro Ser
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	1	5	10	15
Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Lys	Lys	Gln	Asn	20	25	30	
Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	35	40	45	
Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	50	55	60	
His	Leu	Leu														65			

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr	Ala	Trp	Lys	Val	Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	1	5	10	15
Phe	Glu	Met	Gln	Leu	Ala	His	Ile	Leu	Gln	Pro	Ile	Arg	Gln	Ala	Phe	20	25	30	
Pro	Gln	Cys	Thr	Ile	Leu	Gln	Tyr	Met	Asp	Asp	Ile	Leu	Leu	Ala	Ser	35	40	45	

Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu Ala Thr Met Ala Ser
 50 55 60

Leu Ile
 65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu
 1 5 10 15
 Phe Asp Glu Ala Leu His Arg Asp Leu Ala Asp Phe Arg Ile Gln His
 20 25 30
 Pro Asp Leu Ile Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala
 35 40 45
 Thr Ser Glu Leu Asp Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr
 50 55 60
 Leu
 65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Gln Trp Lys Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile
 1 5 10 15
 Cys Gln Leu Val Val Gly Gln Val Leu Glu Pro Leu Arg Leu Lys His
 20 25 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Ala Thr Asn Gly Val Pro Gln Gly Ala Ser Thr Ser Cys Gly Leu
1 5 10 15

Ala Thr Tyr Asn Val Leu Glu Leu Phe Leu Arg Tyr Asp Glu Leu Ile
 20 25 30

Met Tyr Ala Asp Asp Gly Ile Leu Cys Arg Gln Asp Pro Ser Thr Pro
 35 40 45

Asp Phe Ser Val Glu Glu Ala Gly Val Val Gln Glu Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Glu Tyr Leu Arg Met Pro Phe Gly Leu Lys Asn Ala Pro Ala Thr
 1 5 10 15

Phe Gln Arg Cys Met Asn Asp Ile Leu Arg Pro Leu Leu Asn Lys His
 20 25 30

Cys Leu Val Tyr Leu Asp Asp Ile Ile Val Phe Ser Thr Ser Leu Asp
 35 40 45

Glu His Leu Gln Ser Leu Gly Leu Val Phe Glu Lys Leu
 50 55 60

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Glu Phe Cys Arg Leu Pro Phe Gly Leu Arg Asn Ala Ser Ser Ile
 1 5 10 15

Phe Gln Arg Ala Leu Asp Asp Val Leu Arg Glu Gln Ile Gly Lys Ile
 20 25 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys	Lys	Leu	Asn	Lys	Ala	Ile	Tyr	Gly	Leu	Lys	Gln	Ala	Ala	Arg	Cys
1				5					10					15	
Trp	Phe	Arg	Cys	Ile	Tyr	Ile	Leu	Asp	Lys	Gly	Asn	Ile	Asn	Glu	Asn
			20					25					30		
Ile	Tyr	Val	Leu	Leu	Tyr	Val	Asp	Asp	Val	Val	Ile	Ala	Thr	Gly	Asp
		35					40					45			
Met	Thr	Arg	Met	Asn	Asn	Phe	Lys	Arg	Tyr	Leu	Met	Glu	Lys	Phe	
	50					55					60				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys	Leu	Leu	Lys	Lys	Ser	Leu	Tyr	Gly	Leu	Lys	Gln	Ser	Pro	Arg	Gln
1				5					10					15	
Trp	Asn	Ala	Cys	Val	Tyr	Val	Lys	Gln	Val	Ser	Glu	Gln	Glu	His	Leu
			20					25					30		
Tyr	Leu	Leu	Leu	Tyr	Val	Asp	Asp	Met	Leu	Ile	Ala	Gly	Lys	Ser	Lys
		35					40					45			

Ser Glu Ile Asn Lys Val Lys Glu Gln Leu Ser Met Glu Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Arg Leu Lys Lys Ser Leu Tyr Glu Leu Lys Gln Ser Gly Ala Asn
 1 5 10 15
 Trp Tyr Glu Glu Val Arg Gly Trp Ser Cys Val Phe Lys Asn Ser Gln
 20 25 30
 Val Thr Ile Cys Leu Phe Val Asp Asp Met Val Leu Phe Ser Lys Asn
 35 40 45
 Leu Asn Ser Asn Lys Arg Ile Ile Glu Lys Leu Lys Met Gln Tyr
 50 55 60

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "The 2' position of this nucleotide is linked to the 5' position of nucleotide number one of SEQ ID NO:26 of this application."

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 52..58
- (D) OTHER INFORMATION: /product= "This region can hydrogen bond to nucleotides 61-67 of SEQ ID NO:26 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACGCAUGUA GGCAGAUUUG UUGGUUGUGA AUCGCAACCA GUGGCCUUA UGGCAGGA

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "The 2' position of this nucleotide is linked to the 5' position of nucleotide number fifteen of SEQ ID NO:25 of this application."

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 61..67
- (D) OTHER INFORMATION: /product= "This region can hydrogen bond to nucleotides 52-58 of SEQ ID NO:25 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCCTTCGCAC AGCACACCTG CCGTATAGCT CTGAATCAAG GATTTTAGGG AGGCGATTCC	60
TCCTGCC	67

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 418..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGGCCATTNA GATACGGATT TTTCACTTCCT TGACAGTGCA TGACTATGCT GCATGAAATN	60
GCATGATCGA TTGAGGATCG TCTTTGCTCA GATCCGCCAG AACTGGCGGG CTTTGTCTCA	120
TGTCATGCAT GTGCATGAAA ACCACTGCAT AAAGCGGGCA GGCGTGGCGG GGATACGAGC	180
GCGCGCTATC ACCGAAAATA GCCAAAATAC TTCTGGAAAA CAGAAAGTTG AAGTGATATG	240

TTCATAAACA CGCATGTAGG CAGATTTGTT GGTGTGAAT CGCAACCAGT GGCCTTAATG	300
GCAGGAGGAA TCGCCTCCCT AAAATCCTTG ATTCAGAGCT ATACGGCAGG TGTGCTGTGC	360
GAAGGAGTGC CTGCATGCGT TTCTCCTTGG CCTTTTTTCC TCTGGGATGA AGAAGAA	417
ATG ACA AAA ACA TCT AAA CTT GAC GCA CTT AGG GCT GCT ACT TCA CGT Met Thr Lys Thr Ser Lys Leu Asp Ala Leu Arg Ala Ala Thr Ser Arg 1 5 10 15	465
GAA GAC TTG GCT AAA ATT TTA GAT ATT AAG TTG GTA TTT TTA ACT AAC Glu Asp Leu Ala Lys Ile Leu Asp Ile Lys Leu Val Phe Leu Thr Asn 20 25 30	513
GTT CTA TAT AGA ATC GGC TCG GAT AAT CAA TAC ACT CAA TTT ACA ATA Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr Ile 35 40 45	561
CCG AAG AAA GGA AAA GGG GTA AGG ACT ATT TCT GCA CCT ACA GAC CGG Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp Arg 50 55 60	609
TTG AAG GAC ATC CAA CGA AGA ATA TGT GAC TTA CTT TCT GAT TGT AGA Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys Arg 65 70 75 80	657
GAT GAG ATC TTT GCT ATA AGG AAA ATT AGT AAC AAC TAT TCC TTT GGT Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe Gly 85 90 95	705
TTT GAG AGG GGA AAA TCA ATA ATC CTA AAT GCT TAT AAG CAT AGA GGC Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg Gly 100 105 110	753
AAA CAA ATA ATA TTA AAT ATA GAT CTT AAG GAT TTT TTT GAA AGC TTT Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser Phe 115 120 125	801
AAT TTT GGA CGA GTT AGA GGA TAT TTT CTT TCC AAT CAG GAT TTT TTA Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe Leu 130 135 140	849
TTA AAT CCT GTG GTG GCA ACG ACA CTT GCA AAA GCT GCA TGC TAT AAT Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr Asn 145 150 155 160	897
GGA ACC CTC CCC CAA GGA AGT CCA TGT TCT CCT ATT ATC TCA AAT CTA Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn Leu 165 170 175	945
ATT TGC AAT ATT ATG GAT ATG AGA TTA GCT AAG CTG GCT AAA AAA TAT Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys Tyr 180 185 190	993
GGA TGT ACT TAT AGC AGA TAT GCT GAT GAT ATA ACA ATT TCT ACA AAT Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr Asn 195 200 205	1041

AAA AAT ACA TTT CCG TTA GAA ATG GCT ACT GTG CAA CCT GAA GGG GTT Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly Val 210 215 220	1089
GTT TTG GGA AAA GTT TTG GTA AAA GAA ATA GAA AAC TCT GGA TTC GAA Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe Glu 225 230 235 240	1137
ATA AAT GAT TCA AAG ACT AGG CTT ACG TAT AAG ACA TCA AGG CAA GAA Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln Glu 245 250 255	1185
GTA ACG GGA CTT ACA GTT AAC AGA ATC GTT AAT ATT GAT AGA TGT TAT Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys Tyr 260 265 270	1233
TAT AAA AAA ACT CGG GCG TTG GCA CAT GCT TTG TAT CGT ACA GGT GAA Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly Glu 275 280 285	1281
TAT AAA GTG CCA GAT GAA AAT GGT GTT TTA GTT TCA GGA GGT CTG GAT Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu Asp 290 295 300	1329
AAA CTT GAG GGG ATG TTT GGT TTT ATT GAT CAA GTT GAT AAG TTT AAC Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe Asn 305 310 315 320	1377
AAT ATA AAG AAA AAA CTG AAC AAG CAA CCT GAT AGA TAT GTA TTG ACT Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu Thr 325 330 335	1425
AAT GCG ACT TTG CAT GGT TTT AAA TTA AAG TTG AAT GCG CGA GAA AAA Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu Lys 340 345 350	1473
GCA TAT AGT AAA TTT ATT TAC TAT AAA TTT TTT CAT GGC AAC ACC TGT Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr Cys 355 360 365	1521
CCT ACG ATA ATT ACA GAA GGG AAG ACT GAT CGG ATA TAT TTG AAG GCT Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys Ala 370 375 380	1569
GCT TTG CAT TCT TTG GAG ACA TCA TAT CCT GAG TTG TTT AGA GAA AAA Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu Lys 385 390 395 400	1617
ACA GAT AGT AAA AAG AAA GAA ATA AAT CTT AAT ATA TTT AAA TCT AAT Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser Asn 405 410 415	1665
GAA AAG ACC AAA TAT TTT TTA GAT CTT TCT GGG GGA ACT GCA GAT CTG Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp Leu 420 425 430	1713

AAA AAA TTT GTA GAG CGT TAT AAA AAT AAT TAT GCT TCT TAT TAT GGT Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr Gly 435 440 445	1761
TCT GTT CCA AAA CAG CCA GTG ATT ATG GTT CTT GAT AAT GAT ACA GGT Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr Gly 450 455 460	1809
CCA AGC GAT TTA CTT AAT TTT CTG CGC AAT AAA GTT AAA AGC TGC CCA Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys Pro 465 470 475 480	1857
GAC GAT GTA ACT GAA ATG AGA AAG ATG AAA TAT ATT CAT GTT TTC TAT Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe Tyr 485 490 495	1905
AAT TTA TAT ATA GTT CTC ACA CCA TTG AGT CCT TCC GGC GAA CAA ACT Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln Thr 500 505 510	1953
TCA ATG GAG GAT CTT TTC CCT AAA GAT ATT TTA GAT ATC AAG ATT GAT Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile Asp 515 520 525	2001
GGT AAG AAA TTC AAC AAA AAT AAT GAT GGA GAC TCA AAA ACG GAA TAT Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu Tyr 530 535 540	2049
GGG AAG CAT ATT TTT TCC ATG AGG GTT GTT AGA GAT AAA AAG CGG AAA Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg Lys 545 550 555 560	2097
ATA GAT TTT AAG GCA TTT TGT TGT ATT TTT GAT GCT ATA AAA GAT ATA Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp Ile 565 570 575	2145
AAG GAA CAT TAT AAA TTA ATG TTA AAT AGC TAATGAACAG CCCTAACGTT Lys Glu His Tyr Lys Leu Met Leu Asn Ser 580 585	2195
ATGAACGCTA AGGCTGATTT TTCGTAAAA TTTATATGGT TTGAATTGTA ATATATTATC	2255
TTCAAGCCAT TTATTTAATT CCTGCATCCT TTTCTGTAAG GGTATTAATT CGTTCCTCAC	2315
AAACACTAAA CTCGCTTTTT CCACATCCCC AAACCCCCCT AACATTATTC GGCATAATCC	2375
CCATCATTTG CGGTGGCACA CGATGCGCTG CCATCATGTC ATCGCGGC	2423

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 586 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Thr Lys Thr Ser Lys Leu Asp Ala Leu Arg Ala Ala Thr Ser Arg
 1           5           10           15

Glu Asp Leu Ala Lys Ile Leu Asp Ile Lys Leu Val Phe Leu Thr Asn
          20           25           30

Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr Ile
          35           40           45

Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp Arg
          50           55           60

Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys Arg
          65           70           75           80

Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe Gly
          85           90           95

Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg Gly
          100          105          110

Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser Phe
          115          120          125

Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe Leu
          130          135          140

Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr Asn
          145          150          155          160

Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn Leu
          165          170          175

Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys Tyr
          180          185          190

Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr Asn
          195          200          205

Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly Val
          210          215          220

Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe Glu
          225          230          235          240

Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln Glu
          245          250          255

Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys Tyr
          260          265          270

Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly Glu
          275          280          285

Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu Asp
          290          295          300

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Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe Asn
 305 310 315 320
 Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu Thr
 325 330 335
 Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu Lys
 340 345 350
 Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr Cys
 355 360 365
 Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys Ala
 370 375 380
 Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu Lys
 385 390 395 400
 Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser Asn
 405 410 415
 Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp Leu
 420 425 430
 Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr Gly
 435 440 445
 Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr Gly
 450 455 460
 Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys Pro
 465 470 475 480
 Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe Tyr
 485 490 495
 Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln Thr
 500 505 510
 Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile Asp
 515 520 525
 Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu Tyr
 530 535 540
 Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg Lys
 545 550 555 560
 Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp Ile
 565 570 575
 Lys Glu His Tyr Lys Leu Met Leu Asn Ser
 580 585

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
1           5           10           15

Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
20           25           30

Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
35           40           45

Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys
50           55           60

Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu
65           70           75           80

Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser
85           90           95

Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp
100          105          110

Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
115          120          125

Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp
130          135          140

Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu
145          150          155          160

Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
165          170          175

Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
180          185          190

Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
195          200          205

Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu
210          215          220

Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys
225          230          235          240

```

Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn		
				245					250					255			
Trp	Ala	Ser	Gln	Ile	Tyr	Pro	Gly	Ile	Lys	Val	Arg	Gln	Leu	Cys	Lys		
			260					265					270				
Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	Val	Ile	Pro	Leu	Thr	Glu		
		275					280					285					
Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro		
	290					295					300						
Val	His	Gly	Val	Tyr	Tyr	Asp	Pro	Ser	Lys	Asp	Leu	Ile	Ala	Glu	Ile		
305					310					315					320		
Gln	Lys	Gln	Gly	Gln	Gly	Gln	Trp	Thr	Tyr	Gln	Ile	Tyr	Gln	Glu	Pro		
				325					330					335			
Phe	Lys	Asn	Leu	Lys	Thr	Gly	Lys	Tyr	Ala	Arg	Met	Arg	Gly	Ala	His		
			340					345					350				
Thr	Asn	Asp	Val	Lys	Gln	Leu	Thr	Glu	Ala	Val	Gln	Lys	Ile	Thr	Thr		
		355					360					365					
Glu	Ser	Ile	Val	Ile	Trp	Gly	Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile		
	370					375					380						
Gln	Lys	Glu	Thr	Trp	Glu	Thr	Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr		
385					390					395					400		
Trp	Ile	Pro	Glu	Trp	Glu	Phe	Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu		
				405					410					415			
Trp	Tyr	Gln	Leu	Glu	Lys	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr		
			420					425					430				
Val	Asp	Gly	Ala	Ala	Asn	Arg	Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr		
		435					440					445					
Val	Thr	Asn	Lys	Gly	Arg	Gln	Lys	Val	Val	Pro	Leu	Thr	Asn	Thr	Thr		
	450					455					460						
Asn	Gln	Lys	Thr	Glu	Leu	Gln	Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser		
465					470					475					480		
Gly	Leu	Glu	Val	Asn	Ile	Val	Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gln	Ile		
				485					490					495			
Ile	Gln	Ala	Gln	Pro	Asp	Lys	Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile		
			500					505					510				
Ile	Glu	Gln	Leu	Ile	Lys	Lys	Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro		
	515						520					525					
Ala	His	Lys	Gly	Ile	Gly	Gly	Asn	Glu	Gln	Val	Asp	Lys	Leu	Val	Ser		
	530					535					540						

Ala Gly
545

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg	Pro	Trp	Ala	Arg	Thr	Pro	Pro	Lys	Ala	Pro	Arg	Asn	Gln	Pro	Val	1	5	10	15
Pro	Phe	Lys	Pro	Glu	Arg	Leu	Gln	Ala	Leu	Gln	His	Leu	Val	Arg	Lys	20	25	30	
Ala	Leu	Glu	Ala	Gly	His	Ile	Glu	Pro	Tyr	Thr	Gly	Pro	Gly	Asn	Asn	35	40	45	
Pro	Val	Phe	Pro	Val	Lys	Lys	Ala	Asn	Gly	Thr	Trp	Arg	Phe	Ile	His	50	55	60	
Asp	Leu	Arg	Ala	Thr	Asn	Ser	Leu	Thr	Ile	Asp	Leu	Ser	Ser	Ser	Ser	65	70	75	80
Pro	Gly	Pro	Pro	Asp	Leu	Ser	Ser	Leu	Pro	Thr	Thr	Leu	Ala	His	Leu	85	90	95	
Gln	Thr	Ile	Asp	Leu	Arg	Asp	Ala	Phe	Phe	Gln	Ile	Pro	Leu	Pro	Lys	100	105	110	
Gln	Phe	Gln	Pro	Tyr	Phe	Ala	Phe	Thr	Val	Pro	Gln	Gln	Cys	Asn	Tyr	115	120	125	
Gly	Pro	Gly	Thr	Arg	Tyr	Ala	Trp	Lys	Val	Leu	Pro	Gln	Gly	Phe	Lys	130	135	140	
Asn	Ser	Pro	Thr	Leu	Phe	Glu	Met	Gln	Leu	Ala	His	Ile	Leu	Gln	Pro	145	150	155	160
Ile	Arg	Gln	Ala	Phe	Pro	Gln	Cys	Thr	Ile	Leu	Gln	Tyr	Met	Asp	Asp	165	170	175	
Ile	Leu	Leu	Ala	Ser	Pro	Ser	His	Glu	Asp	Leu	Leu	Leu	Leu	Ser	Glu	180	185	190	
Ala	Thr	Met	Ala	Ser	Leu	Ile	Ser	His	Gly	Leu	Pro	Val	Ser	Glu	Asn	195	200	205	

Lys Thr Gln Gln Thr Pro Gly Thr Ile Lys Phe Leu Gly Gln Ile Ile
 210 215 220
 Ser Pro Asn His Leu Thr Tyr Asp Ala Val Pro Thr Val Pro Ile Arg
 225 230 235 240
 Ser Arg Trp Ala Leu Pro Glu Leu Gln Ala Leu Leu Gly Glu Ile Gln
 245 250 255
 Trp Val Ser Lys Gly Thr Pro Thr Leu Arg Gln Pro Leu His Ser Leu
 260 265 270
 Tyr Cys Ala Leu Gln Arg His Thr Asp Pro Arg Asp Gln Ile Tyr Leu
 275 280 285
 Asn Pro Ser Gln Val Gln Ser Leu Val Gln Leu Arg Gln Ala Leu Ser
 290 295 300
 Gln Asn Cys Arg Ser Arg Leu Val Gln Thr Leu Pro Leu Leu Gly Ala
 305 310 315 320
 Ile Met Leu Thr Leu Thr Gly Thr Thr Thr Val Val Phe Gln Ser Lys
 325 330 335
 Glu Gln Trp Pro Leu Val Trp Leu His Ala Pro Leu Pro His Thr Ser
 340 345 350
 Gln Cys Pro Trp Gly Gln Leu Leu Ala Ser Ala Val Leu Leu Leu Asp
 355 360 365
 Lys Tyr Thr Leu Gln Ser Tyr Gly Leu Leu Cys Gln Thr Ile His His
 370 375 380
 Asn Ile Ser Thr Gln Thr Phe Asn Gln Phe Ile Gln Thr Ser Asp His
 385 390 395 400
 Pro Ser Val Pro Ile Leu Leu His His Ser His Arg Phe Lys Asn Leu
 405 410 415
 Gly Ala Gln Thr Gly Glu Leu Trp Asn Thr Phe Leu Lys Thr Ala Ala
 420 425 430
 Pro Leu Ala Pro Val Lys Ala Leu Met Pro Val Phe Thr Leu Ser Pro
 435 440 445
 Val Ile Ile Asn Thr Ala Pro Cys Leu Phe Ser Asp Gly Ser Thr Ser
 450 455 460
 Arg Ala Ala Tyr Ile Leu Trp Asp Lys Gln Ile Leu Ser Gln Arg Ser
 465 470 475 480
 Phe Pro Leu Pro Pro Pro His Lys Ser Ala Gln Arg Ala Glu Leu Leu
 485 490 495
 Gly Leu Leu His Gly Leu Ser Ser Ala Arg Ser Trp Arg Cys Leu Asn
 500 505 510

Ile Phe Leu Asp Ser Lys Tyr Leu Tyr His Tyr Leu Arg Thr Leu Ala
 515 520 525
 Leu Gly Thr Phe Gln Gly Arg Ser Ser Gln Ala Pro Phe Gln Ala Leu
 530 535 540
 Leu Pro Arg Leu Leu Ser Arg Lys Val Val Tyr Leu His His Val Arg
 545 550 555 560
 Ser His Thr Asn Leu Pro Asp Pro Ile Ser Arg Leu Asn Ala Leu Thr
 565 570 575
 Asp Ala

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr
 1 5 10 15
 Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp
 20 25 30
 Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys
 35 40 45
 Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe
 50 55 60
 Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg
 65 70 75 80
 Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser
 85 90 95
 Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe
 100 105 110
 Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr
 115 120 125
 Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn
 130 135 140

Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys
 145 150 155 160
 Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr
 165 170 175
 Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly
 180 185 190
 Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe
 195 200 205
 Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln
 210 215 220
 Glu Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys
 225 230 235 240
 Tyr Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly
 245 250 255
 Glu Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu
 260 265 270
 Asp Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe
 275 280 285
 Asn Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu
 290 295 300
 Thr Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu
 305 310 315 320
 Lys Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr
 325 330 335
 Cys Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys
 340 345 350
 Ala Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu
 355 360 365
 Lys Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser
 370 375 380
 Asn Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp
 385 390 395 400
 Leu Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr
 405 410 415
 Gly Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr
 420 425 430
 Gly Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys
 435 440 445


```

Pro Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe
 450                      455                      460

Tyr Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln
465                      470                      475                      480

Thr Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile
                      485                      490                      495

Asp Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu
                      500                      505                      510

Tyr Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg
                      515                      520                      525

Lys Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp
                      530                      535                      540

Ile Lys Glu His Tyr Lys Leu Met Leu Asn Ser
545                      550                      555

```

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln
 1                      5                      10                      15

Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala
                20                      25                      30

Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val
    35                      40                      45

Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
    50                      55                      60

Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
    65                      70                      75                      80

Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg
                85                      90                      95

Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr
    100                      105                      110

```

Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe
 115 120 125
 Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg Ala Leu Pro Gln
 130 135 140
 Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu
 145 150 155 160
 Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr
 165 170 175
 Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser
 180 185 190
 Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu
 195 200 205
 Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro
 210 215 220
 Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly
 225 230 235 240
 Leu Val Val

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val
 1 5 10 15
 Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser
 20 25 30
 Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val
 35 40 45
 Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
 50 55 60
 Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
 65 70 75 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg	His	Tyr	Ser	Ile	His	Arg	Pro	Arg	Glu	Arg	Val	Arg	His	Tyr	Val
1				5					10					15	
Thr	Phe	Ala	Val	Pro	Lys	Arg	Ser	Gly	Gly	Val	Arg	Leu	Leu	His	Ala
			20					25					30		
Pro	Lys	Arg	Arg	Leu	Lys	Ala	Leu	Gln	Arg	Arg	Met	Leu	Ala	Leu	Leu
		35					40					45			

```

Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val Pro Gly
 50                      55                      60

Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg Val Val
65                      70                      75                      80

Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe Ala Arg
                        85                      90                      95

Val Arg Gly Leu Leu Lys Ala Leu Gly Tyr Gly Tyr Pro Val Ala Ala
                        100                    105                    110

Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val Glu Leu
      115                      120                      125

Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys Val Gln
      130                      135                      140

Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu
145                      150                      155                      160

Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr Tyr Thr
                        165                      170                      175

Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr Ala Leu
                        180                      185                      190

Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu Gly Phe
      195                      200                      205

Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly Ala Gln
      210                    215                      220

Arg Val Thr Gly Val Thr Val
225                      230

```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Phe Leu Thr Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr
1                      5                      10                      15

Gln Phe Thr Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala
      20                      25                      30

```

Pro Thr Asp Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu
 35 40 45
 Ser Asp Cys Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn
 50 55 60
 Tyr Ser Phe Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr
 65 70 75 80
 Lys His Arg Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe
 85 90 95
 Phe Glu Ser Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn
 100 105 110
 Gln Asp Phe Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala
 115 120 125
 Ala Cys Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile
 130 135 140
 Ile Ser Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu
 145 150 155 160
 Ala Lys Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr
 165 170 175
 Ile Ser Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln
 180 185 190
 Pro Glu Gly Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn
 195 200 205
 Ser Gly Phe Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr
 210 215 220
 Ser Arg Gln Glu Val Thr Gly Leu Thr Val
 225 230

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe Arg Tyr Arg
 1 5 10 15

```

Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met Arg Thr Ile
      20                      25                      30

Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp Val Leu Arg
      35                      40                      45

Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile Gly Phe Glu
      50                      55                      60

Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile Gly Ala Asn
      65                      70                      75                      80

Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser Leu Thr Ala
      85                      90                      95

Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn Arg Leu Ile
      100                     105                     110

Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu Leu Pro Gln
      115                     120                     125

Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys Ser Lys Leu
      130                     135                     140

Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu Ile Tyr Thr
      145                     150                     155                     160

Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met Lys Lys Val
      165                     170                     175

Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser Glu Gly Leu
      180                     185                     190

Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg Ser Gln Arg
      195                     200                     205

Lys Val Thr Gly Leu Val Ile
      210                     215

```

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Thr Lys Gly Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys
1      5      10      15

```

Lys	Trp	Asp	Ile	Ala	Lys	Lys	Lys	Gly	Gly	Met	Arg	Thr	Ile	Tyr	His	20	25	30	
Pro	Ser	Ser	Lys	Val	Lys	Leu	Ile	Gln	Tyr	Trp	Leu	Met	Asn	Asn	Val	35	40	45	
Phe	Ser	Lys	Leu	Pro	Met	His	Asn	Ala	Ala	Tyr	Ala	Phe	Val	Lys	Asn	50	55	60	
Arg	Ser	Ile	Lys	Ser	Asn	Ala	Leu	Leu	His	Ala	Glu	Ser	Lys	Asn	Lys	65	70	75	80
Tyr	Tyr	Val	Lys	Ile	Asp	Leu	Lys	Asp	Phe	Phe	Pro	Ser	Ile	Lys	Phe	85	90	95	
Thr	Asp	Phe	Glu	Tyr	Ala	Phe	Thr	Arg	Tyr	Arg	Asp	Arg	Ile	Glu	Phe	100	105	110	
Thr	Thr	Glu	Tyr	Asp	Leu	Glu	Leu	Leu	Gln	Leu	Ile	Lys	Thr	Ile	Cys	115	120	125	
Phe	Ile	Ser	Asp	Ser	Thr	Leu	Pro	Ile	Gly	Phe	Pro	Thr	Ser	Pro	Leu	130	135	140	
Ile	Ala	Asn	Phe	Val	Ala	Arg	Glu	Leu	Asp	Glu	Lys	Leu	Thr	Gln	Lys	145	150	155	160
Leu	Asn	Ala	Ile	Asp	Lys	Leu	Asn	Ala	Thr	Tyr	Thr	Arg	Tyr	Ala	Asp	165	170	175	
Asp	Ile	Ile	Val	Ser	Thr	Asn	Met	Lys	Gly	Ala	Ser	Lys	Leu	Ile	Leu	180	185	190	
Asp	Cys	Phe	Lys	Arg	Thr	Met	Lys	Glu	Ile	Gly	Pro	Asp	Phe	Lys	Ile	195	200	205	
Asn	Ile	Lys	Lys	Phe	Lys	Ile	Cys	Ser	Ala	Ser	Gly	Gly	Ser	Ile	Val	210	215	220	
Val	Thr	Gly	Leu	Lys	Val											225	230		

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile Gln Arg Leu His Ala Leu Ser Asn His Ala Gly Arg His Tyr Arg
 1 5 10 15
 Arg Ile Ile Leu Ser Lys Arg His Gly Gly Gln Arg Leu Val Leu Ala
 20 25 30
 Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys Asn Val
 35 40 45
 Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg Pro Gly
 50 55 60
 Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro Gln Ile
 65 70 75 80
 Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp Leu Gln
 85 90 95
 Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val Val Thr
 100 105 110
 Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln Gly Ala
 115 120 125
 Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe Asp Glu
 130 135 140
 Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr Arg Tyr
 145 150 155 160
 Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln Val Lys
 165 170 175
 Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu Asn Lys
 180 185 190
 Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val Thr Gly
 195 200 205
 Ile Val Val
 210

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 279..1559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTCCGAGCCC GCCTCCGAGG ACGCGCTCGC GGCCCGGGCG GCGGGGGCGG ACGCGCGGCG	60
GCGGCCCACG GAGACGCTTG ACCCGGGAGA CGACGAATGA CGATAACGGC AGGTGCTCTC	120
GGGAGAGGCC AGGGCTCGCA GATGAGCCAT GAGTACCGCG GTGTTTCGCC GCGGGGGTGT	180
TCTGTCCCCA TCTCTTCGCC AGGGTCCCAG CGTACGCAAC GCAGGGAGCC CCGGGTCCAA	240
CGCCTCGCAG GTCGTCCCCT GGCCTCTTCC GGAGCACC ATG AGC TGG TTC GAC	293
Met Ser Trp Phe Asp	
1 5	
ACC ACC CTC TCC CGG CTC AAG GGG TTG TTC AGC CGT CCC GTG ACA CGA	341
Thr Thr Leu Ser Arg Leu Lys Gly Leu Phe Ser Arg Pro Val Thr Arg	
10 15 20	
AGC ACC ACC GGG CTG GAC GTG CCG CTG GAT GCC CAC GGA CGT CCC CAG	389
Ser Thr Thr Gly Leu Asp Val Pro Leu Asp Ala His Gly Arg Pro Gln	
25 30 35	
GAC GTC GTG ACG GAG ACG GTC TCC ACG TCG GGC CCC CTG AAG CCA GGG	437
Asp Val Val Thr Glu Thr Val Ser Thr Ser Gly Pro Leu Lys Pro Gly	
40 45 50	
CAC CTG CGA CAG GTC CGC CGG GAT GCG CGG CTG CTC CCC AAG GGC GTC	485
His Leu Arg Gln Val Arg Arg Asp Ala Arg Leu Leu Pro Lys Gly Val	
55 60 65	
CGC CGC TAC ACC CCG GGC CGG AAG AAG TGG ATG GAG GCC GCC GAG GCC	533
Arg Arg Tyr Thr Pro Gly Arg Lys Lys Trp Met Glu Ala Ala Glu Ala	
70 75 80 85	
CGG CGG CTG TTC TCC GCC ACG CTG CGC ACG CGG AAC CGG AAC CTG AGG	581
Arg Arg Leu Phe Ser Ala Thr Leu Arg Thr Arg Asn Arg Asn Leu Arg	
90 95 100	
GAC TTG CTG CCC GAC GAG GCA CAG CTG GCG CGC TAC GGC CTG CCG GTC	629
Asp Leu Leu Pro Asp Glu Ala Gln Leu Ala Arg Tyr Gly Leu Pro Val	
105 110 115	
TGG CGC ACG GAA GAG GAC GTG GCA GCG GCC CTG GGC GTC TCG GTG GGC	677
Trp Arg Thr Glu Glu Asp Val Ala Ala Ala Leu Gly Val Ser Val Gly	
120 125 130	
GTG CTC CGC CAC TAC AGC ATC CAC CGC CCG CGC GAG CGG GTG CGG CAC	725
Val Leu Arg His Tyr Ser Ile His Arg Pro Arg Glu Arg Val Arg His	
135 140 145	
TAC GTG ACC TTC GCC GTG CCC AAG CGC TCC GGA GGC GTC CGG CTG CTG	773
Tyr Val Thr Phe Ala Val Pro Lys Arg Ser Gly Gly Val Arg Leu Leu	
150 155 160 165	

CAT GCG CCC AAG CGG CGC CTG AAG GCC CTG CAA CGC CGG ATG CTG GCG	821
His Ala Pro Lys Arg Arg Leu Lys Ala Leu Gln Arg Arg Met Leu Ala	
170 175 180	
CTC CTG GTG TCG AAG CTC CCC GTG AGT CCA CAG GCC CAT GGC TTC GTG	869
Leu Leu Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val	
185 190 195	
CCC GGC CGC TCC ATC AAG ACG GGC GCC GCG CCG CAC GTG GGC CGG CGG	917
Pro Gly Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg	
200 205 210	
GTG GTC CTG AAG CTG GAC CTG AAG GAC TTC TTC CCC TCC GTC ACC TTC	965
Val Val Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe	
215 220 225	
GCG CGG GTG CGA GGG CTG CTC ATC GCC CTG GGC TAC GGC TAT CCC GTG	1013
Ala Arg Val Arg Gly Leu Leu Ile Ala Leu Gly Tyr Gly Tyr Pro Val	
230 235 240 245	
GCG GCC ACG CTC GCG GTG CTG ATG ACG GAG TCC GAG CGC CAG CCC GTG	1061
Ala Ala Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val	
250 255 260	
GAG CTG GAG GGC ATC CTC TTC CAC GTT CCC GTG GGC CCA CGC GTC TGC	1109
Glu Leu Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys	
265 270 275	
GTG CAG GGC GCC CCC ACG AGC CCC GCC CTG TGC AAC GCG GTG CTG CTG	1157
Val Gln Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu	
280 285 290	
CGA CTG GAC CGG CGG CTG GCG GGA CTG GCG CGT CGG TAC GGC TAC ACG	1205
Arg Leu Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr	
295 300 305	
TAC ACG CGC TAC GCG GAT GAC CTC ACC TTC TCC GGC GAC GAC GTC ACG	1253
Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr	
310 315 320 325	
GCG CTG GAG CGA GTC CGC GCG CTG GCC GCG CGG TAC GTG CAG GAG GAA	1301
Ala Leu Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu	
330 335 340	
GGC TTC GAG GTC AAC CGC GAG AAG ACC CGC GTG CAG CGC CGG GGC GGT	1349
Gly Phe Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly	
345 350 355	
GCC CAG CGC GTC ACT GGC GTC ACC GTG AAT ACG ACG CTG GGC TTG TCA	1397
Ala Gln Arg Val Thr Gly Val Thr Val Asn Thr Thr Leu Gly Leu Ser	
360 365 370	
CGC GAG GAG CGG CCG CGG CTC CGG GCG ATG CTG CAC CAG GAG GCG CGG	1445
Arg Glu Glu Arg Pro Arg Leu Arg Ala Met Leu His Gln Glu Ala Arg	
375 380 385	

TCG GAG GAC GTC GAG GCA CAC CGC GCG CAC CTC GAC GGC CTC CTG GCC	1493
Ser Glu Asp Val Glu Ala His Arg Ala His Leu Asp Gly Leu Leu Ala	
390 395 400 405	
TAC GTG AAG ATG CTC AAC CCG GAG CAG GCG GAG CGG CTC GCT CGC CGG	1541
Tyr Val Lys Met Leu Asn Pro Glu Gln Ala Glu Arg Leu Ala Arg Arg	
410 415 420	
CGC AAG CCG CGC GGG ACG TGAGCGAGGG CTCAGCTCCG GATGGGCCAG	1589
Arg Lys Pro Arg Gly Thr	
425	
GGCCTGTCAC GCGTCCCGGC CTCCAGTTG TCATGGCGGC CGTCCAGTA C	1640

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Ser	Trp	Phe	Asp	Thr	Thr	Leu	Ser	Arg	Leu	Lys	Gly	Leu	Phe	Ser	
1				5					10					15		
Arg	Pro	Val	Thr	Arg	Ser	Thr	Thr	Gly	Leu	Asp	Val	Pro	Leu	Asp	Ala	
			20					25					30			
His	Gly	Arg	Pro	Gln	Asp	Val	Val	Thr	Glu	Thr	Val	Ser	Thr	Ser	Gly	
		35				40						45				
Pro	Leu	Lys	Pro	Gly	His	Leu	Arg	Gln	Val	Arg	Arg	Asp	Ala	Arg	Leu	
	50					55					60					
Leu	Pro	Lys	Gly	Val	Arg	Arg	Tyr	Thr	Pro	Gly	Arg	Lys	Lys	Trp	Met	
	65				70					75					80	
Glu	Ala	Ala	Glu	Ala	Arg	Arg	Leu	Phe	Ser	Ala	Thr	Leu	Arg	Thr	Arg	
				85					90					95		
Asn	Arg	Asn	Leu	Arg	Asp	Leu	Leu	Pro	Asp	Glu	Ala	Gln	Leu	Ala	Arg	
			100					105					110			
Tyr	Gly	Leu	Pro	Val	Trp	Arg	Thr	Glu	Glu	Asp	Val	Ala	Ala	Ala	Leu	
		115				120						125				
Gly	Val	Ser	Val	Gly	Val	Leu	Arg	His	Tyr	Ser	Ile	His	Arg	Pro	Arg	
	130					135					140					
Glu	Arg	Val	Arg	His	Tyr	Val	Thr	Phe	Ala	Val	Pro	Lys	Arg	Ser	Gly	
	145				150					155					160	
Gly	Val	Arg	Leu	Leu	His	Ala	Pro	Lys	Arg	Arg	Leu	Lys	Ala	Leu	Gln	
			165					170						175		

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Arg Arg Met Leu Ala Leu Leu Val Ser Lys Leu Pro Val Ser Pro Gln
      180                      185                      190

Ala His Gly Phe Val Pro Gly Arg Ser Ile Lys Thr Gly Ala Ala Pro
      195                      200                      205

His Val Gly Arg Arg Val Val Leu Lys Leu Asp Leu Lys Asp Phe Phe
      210                      215                      220

Pro Ser Val Thr Phe Ala Arg Val Arg Gly Leu Leu Ile Ala Leu Gly
      225                      230                      235                      240

Tyr Gly Tyr Pro Val Ala Ala Thr Leu Ala Val Leu Met Thr Glu Ser
      245                      250                      255

Glu Arg Gln Pro Val Glu Leu Glu Gly Ile Leu Phe His Val Pro Val
      260                      265                      270

Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser Pro Ala Leu Cys
      275                      280                      285

Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala Gly Leu Ala Arg
      290                      295                      300

Arg Tyr Gly Tyr Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser
      305                      310                      315                      320

Gly Asp Asp Val Thr Ala Leu Glu Arg Val Arg Ala Leu Ala Ala Arg
      325                      330                      335

Tyr Val Gln Glu Glu Gly Phe Glu Val Asn Arg Glu Lys Thr Arg Val
      340                      345                      350

Gln Arg Arg Gly Gly Ala Gln Arg Val Thr Gly Val Thr Val Asn Thr
      355                      360                      365

Thr Leu Gly Leu Ser Arg Glu Glu Arg Pro Arg Leu Arg Ala Met Leu
      370                      375                      380

His Gln Glu Ala Arg Ser Glu Asp Val Glu Ala His Arg Ala His Leu
      385                      390                      395                      400

Asp Gly Leu Leu Ala Tyr Val Lys Met Leu Asn Pro Glu Gln Ala Glu
      405                      410                      415

Arg Leu Ala Arg Arg Arg Lys Pro Arg Gly Thr
      420                      425

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(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3060 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 763..2202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCATTCCG GCGCTCGGGC TGC GCGAGGG CCCGTGCGAG CACATGATGG CGCTGCGGCT	60
CGTCCAGGTC CGGCACCGCG CCGAGCAGGA AGCACTGCGT CAGACCCCCG CGGGCCGCCA	120
GCTCATCCGC GCGGAGACGC GCTCCTACGT GCGGCGCGAG CCCTCCGGCC AGGAGCAGGT	180
GTACCGCGTC TCATTGGATG GGAAAGTGGT GCGGTTGGAG TGGGGCCCCC GCCAGGGGGA	240
GTCCCGCCGG CAGAAGCTCT GGTTCGACAC GGACGCCGAG GCGCGCACCG CCTACTTCAC	300
GCGCCTGGAG TCCTTGGCCG CGGAGGGATA TATCGATGCG GCTGCTTCAA TGATGTAGAA	360
CACGCAAGCC ACGGGGCCGC GGGCGCGCGG CGGAAAGGCA GGTGCGACGG AACGACAGAC	420
ACTCGTGCGA GCGACCGAGA GAGGTCCCAA GCCATCAGCC TCAGCGCCTC GAGCGCGAGA	480
GCGGCGTTGC GCCGCTCTGG TTGAATTGCA GGACACTCTC CGCAAGGTAG CCTGTTCTTG	540
GCTCTCTTCC CTCCGGTGAG TACCTCTCCG GCCGGGGAGC TGAACCAACG ACGCAACCGC	600
CGTTTCCCCG GCCGGAGAGG TACTCACCGG AGGGGAGAGC CGGTGAGGCT ACCGTGCCCC	660
AGGTGAGAAG GTGGTGCCCTT CGGGCCTCCC TCGACCGCTC GCGCTCCGTC GCCCTGCCCT	720
GCCTCGCCCC CCCACCTTG CTCACCGGCG CCAGGAGCCG TC ATG ACC GCC AAG	774
Met Thr Ala Lys	
1	
CTG GAG TCA CAC GTC CCC GCC GCG CCC CCC GTC TCC GCC GAG GCG CCC	822
Leu Glu Ser His Val Pro Ala Ala Pro Pro Val Ser Ala Glu Ala Pro	
5 10 15 20	
GCC CCC ACC CGT CCC GAT GCC GCG AAG CAG GAG GCC CGC CGC GCC CAC	870
Ala Pro Thr Arg Pro Asp Ala Ala Lys Gln Glu Ala Arg Arg Ala His	
25 30 35	
CAC GAG GCG CTG CGC CTG CGG TGG AAG GCC ATC GAA GAG GCG GGC GGC	918
His Glu Ala Leu Arg Leu Arg Trp Lys Ala Ile Glu Glu Ala Gly Gly	
40 45 50	
ACG GAC GCC TGG GTG CGG CAG CAG CTG GTG GCC AAG GGC GTC GCG GCG	966
Thr Asp Ala Trp Val Arg Gln Gln Leu Val Ala Lys Gly Val Ala Ala	
55 60 65	
GAA GAG GTG GAC TTC GAG TCG CTC AGC GAC AAG CAG AAG GCG GCC TGG	1014
Glu Glu Val Asp Phe Glu Ser Leu Ser Asp Lys Gln Lys Ala Ala Trp	
70 75 80	

AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGG CGC GCG CAG AAG CGC	1062
Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Gln Lys Arg	
85 90 95 100	
CTG GCG TGG GAG GCC TGG AAG GCC ACG CAC ATC CAC CAC CTG GGC GTG	1110
Leu Ala Trp Glu Ala Trp Lys Ala Thr His Ile His His Leu Gly Val	
105 110 115	
GGG GTG CAC TGG GAC GAG GCC GGA GGG CCG GAC AAG TTC GAC GTG GCC	1158
Gly Val His Trp Asp Glu Ala Gly Gly Pro Asp Lys Phe Asp Val Ala	
120 125 130	
GGG CGC GAG GAG CGG GCC AAG GCC AAC GGC TTG CCG GAG GGG TTG GAC	1206
Gly Arg Glu Glu Arg Ala Lys Ala Asn Gly Leu Pro Glu Gly Leu Asp	
135 140 145	
TCG GTC GAG GCG CTG GCC AAA GCG CTG GGC ATC TCC GTG TCG CGC CTG	1254
Ser Val Glu Ala Leu Ala Lys Ala Leu Gly Ile Ser Val Ser Arg Leu	
150 155 160	
CGC TGG TTC TCC TTC CAC CGC GAG GTG GAC ACG GGC ACG CAC TAC CAG	1302
Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln	
165 170 175 180	
ACG TGG GAG ATT CCG AAG CGG GAC GGC GGC AAG CGG ACG CTC ACC GCG	1350
Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala	
185 190 195	
CCG AAG CGG GAG CTC AAG GCC GTG CAG CGC TGG GTG CTC GCG AAC GTG	1398
Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val	
200 205 210	
GTG GAG CGG CTG CCG GTG CAC GGG GCC GCG CAC GGC TTC GTG GCG GGG	1446
Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly	
215 220 225	
CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTG GTG	1494
Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val	
230 235 240	
GTG AAG GTG GAC ATG AAG GAC TTC TTC CCT TCC GTG ACG TGG CCC CGG	1542
Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg	
245 250 255 260	
GTC AAG GGA CTG CTG CGC AAG GGA GGA CTC CCG GAG AAC CTG GCG ACG	1590
Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr	
265 270 275	
CTC CTG GCG CTG CTC TCC ACC GAG GCC CCG CGC GAG GTG GTG CGG TTC	1638
Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe	
280 285 290	
CGG GGA GAG ACG CTG TAC GTG GCC AAG GGC CCT CGC GCG CTG CCC CAG	1686
Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg Ala Leu Pro Gln	
295 300 305	

GGG GCC CCC ACC TCT CCG GCG CTG ACG AAC GCG CTG TGC CTG CGG CTG Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu 310 315 320	1734
GAC AAG CGG CTC TCG GCG CTG TCG AAG CGG CTG GGC TTC ACG TAC ACG Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr 325 330 335 340	1782
CGC TAT GCG GAT GAC CTG ACG TTC TCC TGG CGG CGG GCG AAG AAG TCC Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser 345 350 355	1830
CGG CAG AAG GAA CTC CCC CTG GCG GAT GCG CCG GTG GCG CTG CTC CTG Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu 360 365 370	1878
GCG CGG GTG AAG GGT GTG CTG GAG GCC GAG GGT TTC ACG CTG CAC CCG Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro 375 380 385	1926
GAC AAG ACG CGG GTG CAG CGC AAG GGC AGC CGG CAG CGG GTG ACG GGG Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly 390 395 400	1974
CTC GTG GTG AAC GAG GCC CCC GAG GGC GTT CCG GGT GCC CGG GTG CCC Leu Val Val Asn Glu Ala Pro Glu Gly Val Pro Gly Ala Arg Val Pro 405 410 415 420	2022
CGC GAT GTG GTG CGG CGG CTG CGC GCG GCG ATC CAC AAC CGG GAG CAG Arg Asp Val Val Arg Arg Leu Arg Ala Ala Ile His Asn Arg Glu Gln 425 430 435	2070
GGC AAG CCC GGC CCC ACC GGG GAG ACG CTG GAG CAG CTC AAG GGG CTC Gly Lys Pro Gly Pro Thr Gly Glu Thr Leu Glu Gln Leu Lys Gly Leu 440 445 450	2118
GCG GCC TTC CTT CAC ATG ACG GAC GCG GAG AAG GGC CGC GCC TTC CTG Ala Ala Phe Leu His Met Thr Asp Ala Glu Lys Gly Arg Ala Phe Leu 455 460 465	2166
CGA CGG CTG GAG GCC CTC GAG AAG CGC CAG ACC GCC TGACCCTCAC Arg Arg Leu Glu Ala Leu Glu Lys Arg Gln Thr Ala 470 475 480	2212
TGGTCGTCCG GGGCATCGCA GCGGGCGCCG GGACGGACCG TCACCCCCCA GATCTCCATG	2272
CCATGCTGGG GATTCTGGGC GGTGAAGAAG ACTTCCCAGC CGAGACGGAC GAAGCCCTGC	2332
GGATCCGATG ACTCCTCGCC CGGGGCGATC TCCCGGAGGG GCACCGTTCC GACGTCCGTG	2392
CCATTGCTCA CCCAGGGCTC CCGGCCCCAG CCTTGGGTGT CCGCCGAGAA GAAGAGCAGC	2452
CCGGAGATGG CCGTCAGGTT CTCCGGCGAC GCATCCTCGG GGCCCGGCGC CAAATCCTTC	2512
AGCAGCAGGG TGCCCTTGGC GGTGCCATCG CTGGACCACA GCTCCCGGCC GTGGAGGCTG	2572
TCACTCGCGG CGAAGTAGAG CATCCCATTC AGCGCCTTGA TGGCGCTGGG CGCCGAGCTG	2632

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TCCGGACCCG GCCAGATGTC CTTACCCCGG ACCGTGCCAT GCGACGTGCC ATCGCTGACC 2692
CACAGCTCCT CGCCCTCGGG CTGGCCCCAG AACTCGGGCT CGCCTCCCCC GGCGCTGAAG 2752
AAGATCTTCC CCCCAGAGCGC CGTGAGATCA TCGGATAGA GGCCGGGGAA GAAGCGCAGC 2812
TGCTCGGAGA CGGTGCCTCT GGAGACCAC AGGCTGGCCT CGCCTTCGTC ATTGTCGAGC 2872
AGGAAGAAGA GCACCGAGTC CGCCGCGGTG AACGCGGAGA GGAAGTTGTC CTCGGGGCCC 2932
GTGAAGACAG ACGTGGTGCT GGACAGCCCC AGGCTGCGCC AGATGAACAC CTCGTCATTG 2992
ACGTTGGCCA CGAAGAAGAG CGCATCGCCG ACCCGGGTGA GCCGGCGCGG GCTGGAGCTG 3052
CCGGGCAC 3060

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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Met Thr Ala Lys Leu Glu Ser His Val Pro Ala Ala Pro Pro Val Ser
 1           5           10           15
Ala Glu Ala Pro Ala Pro Thr Arg Pro Asp Ala Ala Lys Gln Glu Ala
          20           25           30
Arg Arg Ala His His Glu Ala Leu Arg Leu Arg Trp Lys Ala Ile Glu
          35           40           45
Glu Ala Gly Gly Thr Asp Ala Trp Val Arg Gln Gln Leu Val Ala Lys
          50           55           60
Gly Val Ala Ala Glu Glu Val Asp Phe Glu Ser Leu Ser Asp Lys Gln
          65           70           75           80
Lys Ala Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg
          85           90           95
Ala Gln Lys Arg Leu Ala Trp Glu Ala Trp Lys Ala Thr His Ile His
          100          105          110
His Leu Gly Val Gly Val His Trp Asp Glu Ala Gly Gly Pro Asp Lys
          115          120          125
Phe Asp Val Ala Gly Arg Glu Glu Arg Ala Lys Ala Asn Gly Leu Pro
          130          135          140
Glu Gly Leu Asp Ser Val Glu Ala Leu Ala Lys Ala Leu Gly Ile Ser
          145          150          155          160

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Arg Ala Phe Leu Arg Arg Leu Glu Ala Leu Glu Lys Arg Gln Thr Ala
 465 470 475 480

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(2..103, 707..1654)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

T TTC GAG AAG CGC CAT ACC AAA CAG GGG ATA CAG ACC AAC CTG ACG	46
Phe Glu Lys Arg His Thr Lys Gln Gly Ile Gln Thr Asn Leu Thr	
1 5 10 15	
CTG AAA GAG GAA AGC TAC GGC GAC TGG CTG CCG AAG TGC GAC GAC CCC	94
Leu Lys Glu Glu Ser Tyr Gly Asp Trp Leu Pro Lys Cys Asp Asp Pro	
20 25 30	
GCA GCA ACA TAACCTCACT CAGACCGGCA ACAGCCGGTC TTTTCCTTTC	143
Ala Ala Thr	
TGGCCATTGC CACAAGGTGA ACAATCCACT GTTCACCCTT CACCGTTTAT TCACCCTTTA	203
TCACTATGAA ATTATTAATA AAAAACCAGA GGTGAACAGT GTGAACAGTA AAACCTGAAA	263
AAACTTTTTTA TCACCCCGCG CATCGCCCGA CTGGACAGAT CCAGAACGAG CAAAAATCAC	323
AAAGGTGACG AGTCGACTGT TCACTCTTCA CCAACTCATC ACCACCTAAC CACATGATAT	383
AAAATGATAA ATAATCGAGG TGAACAGTTA AATGCAAAAA AACTTTTTTCT CAGCTCTTGG	443
ATAAAAGAAA ATTAATTAC ATCAATAGCT TTCCTCTTGA ATCCTCTTGA GGTTCATGAG	503
AGCGTAACAG AGCCAAACCT AGCATTTTAT GGGTTAATAG CCCATCGCGC ATGAGTCATG	563
GTTTCGCCTA GTATTTTAGC TATGCCCGTC GTTCAGTTTCG CTGAGCGGCG GCTGGGGGCC	623
ACCGATCAGC GAACTGATCG ACGTGCTCAA GTAGGTTTGG CTCTTTTAGT CCTCTACCAT	683
CAAGGTGCAT AAGGATATTC TCG ATG CTG ACT CAG CTA AAA AAA AAT GGT	733
Met Leu Thr Gln Leu Lys Lys Asn Gly	
35 40	

ACT GAG GTA TCT AGA GCA ACC GCG TTA TTT TCA TCA TTC GTT GAA AAG Thr Glu Val Ser Arg Ala Thr Ala Leu Phe Ser Ser Phe Val Glu Lys 45 50 55	781
AAC AAA GTA AAA TGT CCT GGT AAT GTA AAA AAA TTC GTC TTT CTG TGT Asn Lys Val Lys Cys Pro Gly Asn Val Lys Lys Phe Val Phe Leu Cys 60 65 70 75	829
GGT GCT AAC AAA AAC AAT GGA GAA CCA TCA GCA AGA CGA TTG GAA TTA Gly Ala Asn Lys Asn Asn Gly Glu Pro Ser Ala Arg Arg Leu Glu Leu 80 85 90	877
ATA AAT TTT TCT GAA AGG TAT TTG AAT AAC TGT CAC TTT TTT CTT GCT Ile Asn Phe Ser Glu Arg Tyr Leu Asn Asn Cys His Phe Phe Leu Ala 95 100 105	925
GAA CTA GTT TTC AAA GAA TTA AGC ACC GAT GAA GAA TCA TTA TCT GAT Glu Leu Val Phe Lys Glu Leu Ser Thr Asp Glu Glu Ser Leu Ser Asp 110 115 120	973
AAT TTA TTA GAT ATC GAA GCT GAC TTA TCT AAA TTA GCT GAT CAT ATT Asn Leu Leu Asp Ile Glu Ala Asp Leu Ser Lys Leu Ala Asp His Ile 125 130 135	1021
ATC ATT GTT TTA GAA AGT TAT TCA TCT TTC ACG GAA CTT GGT GCA TTC Ile Ile Val Leu Glu Ser Tyr Ser Ser Phe Thr Glu Leu Gly Ala Phe 140 145 150 155	1069
GCA TAC AGC AAG CAA TTA CGC AAG AAA TTA ATA ATA GTT AAC AAT ACA Ala Tyr Ser Lys Gln Leu Arg Lys Lys Leu Ile Ile Val Asn Asn Thr 160 165 170	1117
AAA TTT ATA AAT GAG AAA TCA TTT ATA AAT ATG GGA CCA ATA AAG GCT Lys Phe Ile Asn Glu Lys Ser Phe Ile Asn Met Gly Pro Ile Lys Ala 175 180 185	1165
ATT ACT CAG CAA TCA CAA CAA TCT GGT CAT TTC TTA CAT TAT AAA ATG Ile Thr Gln Gln Ser Gln Gln Ser Gly His Phe Leu His Tyr Lys Met 190 195 200	1213
ACA GAA GGT ATT GAA AGT ATA GAG CGC TCT GAT GGG ATT GGC GAA ATA Thr Glu Gly Ile Glu Ser Ile Glu Arg Ser Asp Gly Ile Gly Glu Ile 205 210 215	1261
TTC GAC CCC CTA TAT GAT ATT CTT TCT AAG AAC GAC AGA GCA ATT TCA Phe Asp Pro Leu Tyr Asp Ile Leu Ser Lys Asn Asp Arg Ala Ile Ser 220 225 230 235	1309
AGA ACT TTA AAA AAA GAA GAG TTA GAT CCT TCC AGT AAC TTC AAT AAA Arg Thr Leu Lys Lys Glu Glu Leu Asp Pro Ser Ser Asn Phe Asn Lys 240 245 250	1357
GAC TCA GTA CGA TTT ATT CAT GAC GTA ATT TTT GTA TGT GGT CCT TTG Asp Ser Val Arg Phe Ile His Asp Val Ile Phe Val Cys Gly Pro Leu 255 260 265	1405

CAA CTT AAT GAA CTC ATC GAA ATA ATC ACA AAA ATA TTT GGC ACA GAA Gln Leu Asn Glu Leu Ile Glu Ile Ile Thr Lys Ile Phe Gly Thr Glu 270 275 280	1453
AGC CAT TAC AAA AAA AAT CTT CTA AAG CAC CTT GGT ATT CTA ATA GCT Ser His Tyr Lys Lys Asn Leu Leu Lys His Leu Gly Ile Leu Ile Ala 285 290 295	1501
ATT AGA ATA ATA TCA TGC ACA AAT GGG ATT TAT TAT TCT TTG TAT AAA Ile Arg Ile Ile Ser Cys Thr Asn Gly Ile Tyr Tyr Ser Leu Tyr Lys 300 305 310 315	1549
GAA TAT TAT TTT AAA TAT GAC TTT GAC ATT GAC AAC ATA TCA TCA ATG Glu Tyr Tyr Phe Lys Tyr Asp Phe Asp Ile Asp Asn Ile Ser Ser Met 320 325 330	1597
TTT AAA GTT TTT TTC CTC AAG AAC AAG CCA GAA AGG ATG AGG GTA TAT Phe Lys Val Phe Phe Leu Lys Asn Lys Pro Glu Arg Met Arg Val Tyr 335 340 345	1645
GAG AAT ATA TAGCCTAATT GATTCTCAGA CATTGATGAC TAAGGGATTT Glu Asn Ile 350	1694
GCTTCTGAAG TAATGCGATC ACCTGAGCCG CCAAAAAAAT GGGATATAGC TAAGAAAAAA	1754
GGAGGTATGA GAACAATTTA TCACCCGTCA TCAAAAGTTA AATTAATTCA ATATTGGTTA	1814
ATGAATAATG TTTTTTCGAA GCTCCCAATG CATAATGCTG CATATGCATT TGTTAAAAAC	1874
CGATCAATAA AAAGCAATGC TTTATTACAT GCCGAATCAA AGAATAAGTA TTATGTGAAA	1934
ATAGATCTCA AAGATTTTTT CCCTTCAATA AAATTTACTG ATTTTGAGTA CGCATTCACT	1994
CGTTATCGAG ATCGCATTGA ATTTACTACA GAATATGATA AGGAGTTACT ACAACTTATA	2054
AAAACGATCT GCTTTATATC AGATAGCACT CTCCCTATCG GGTTCCTAC ATCTCCATTA	2114
ATTGCAAACT TTGTGGCAAG AGAACTTGAT GAAAAACTGA CGCAAAACT AAATGCAATT	2174
GATAAACTTA ATGCCACTTA TACACGATAT GCTGATGATA TTATTGTCTC TACAAATATG	2234
AAAGGGGCTA GCAAATTAAT TCTGGATTGT TTTAAAAGAA CAATGAAAGA GATTGGTCCA	2294
GACTTTAAAA TTAACATTAA AAAATTTAAG ATTTGTAGTG CTTCGGGAGG AAGTATAGTA	2354
GTTACCGGAT TGAAAGTTTG CCACGATTTT CATATTACAT TACATAGATC AATGAAAGAT	2414
AAAATAAGAT TGCATCTTTC TCTTTTATCA AAGGGCATAT TAAAAGATGA AGATCATAAT	2474
AAACTTTCTG GTTATATTGC TTATGCAAAA GATATAGACC CTCATTTTTA TACAAACTG	2534
AACAGAAAAT ATTTTCAAGA AATAAAATGG ATTCAGAATC TCCACAACAA AGTTGAATAA	2594
ACTTTATATT TTGGATGCAC CCCAATAACT TCATTGATTA AATTGGGAAC AATATAGGCT	2654
TTTCAGGATG ACCTACACTC TAGAGAATGT GTATACAAAA GTGTATAAGT TATTTTCAAA	2714

CCTATATAAA ATACAGCAAA ATCAATGCAT TGGCGGCATT TTACCACTCC TGTGATCTTC 2774
 CGCCAAAATG CCTC 2788

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe	Glu	Lys	Arg	His	Thr	Lys	Gln	Gly	Ile	Gln	Thr	Asn	Leu	Thr	Leu	1	5	10	15
Lys	Glu	Glu	Ser	Tyr	Gly	Asp	Trp	Leu	Pro	Lys	Cys	Asp	Asp	Pro	Ala	20	25	30	
Ala	Thr	Met	Leu	Thr	Gln	Leu	Lys	Lys	Asn	Gly	Thr	Glu	Val	Ser	Arg	35	40	45	
Ala	Thr	Ala	Leu	Phe	Ser	Ser	Phe	Val	Glu	Lys	Asn	Lys	Val	Lys	Cys	50	55	60	
Pro	Gly	Asn	Val	Lys	Lys	Phe	Val	Phe	Leu	Cys	Gly	Ala	Asn	Lys	Asn	65	70	75	80
Asn	Gly	Glu	Pro	Ser	Ala	Arg	Arg	Leu	Glu	Leu	Ile	Asn	Phe	Ser	Glu	85	90	95	
Arg	Tyr	Leu	Asn	Asn	Cys	His	Phe	Phe	Leu	Ala	Glu	Leu	Val	Phe	Lys	100	105	110	
Glu	Leu	Ser	Thr	Asp	Glu	Glu	Ser	Leu	Ser	Asp	Asn	Leu	Leu	Asp	Ile	115	120	125	
Glu	Ala	Asp	Leu	Ser	Lys	Leu	Ala	Asp	His	Ile	Ile	Ile	Val	Leu	Glu	130	135	140	
Ser	Tyr	Ser	Ser	Phe	Thr	Glu	Leu	Gly	Ala	Phe	Ala	Tyr	Ser	Lys	Gln	145	150	155	160
Leu	Arg	Lys	Lys	Leu	Ile	Ile	Val	Asn	Asn	Thr	Lys	Phe	Ile	Asn	Glu	165	170	175	
Lys	Ser	Phe	Ile	Asn	Met	Gly	Pro	Ile	Lys	Ala	Ile	Thr	Gln	Gln	Ser	180	185	190	
Gln	Gln	Ser	Gly	His	Phe	Leu	His	Tyr	Lys	Met	Thr	Glu	Gly	Ile	Glu	195	200	205	
Ser	Ile	Glu	Arg	Ser	Asp	Gly	Ile	Gly	Glu	Ile	Phe	Asp	Pro	Leu	Tyr	210	215	220	

Asp Ile Leu Ser Lys Asn Asp Arg Ala Ile Ser Arg Thr Leu Lys Lys
 225 230 235 240
 Glu Glu Leu Asp Pro Ser Ser Asn Phe Asn Lys Asp Ser Val Arg Phe
 245 250 255
 Ile His Asp Val Ile Phe Val Cys Gly Pro Leu Gln Leu Asn Glu Leu
 260 265 270
 Ile Glu Ile Ile Thr Lys Ile Phe Gly Thr Glu Ser His Tyr Lys Lys
 275 280 285
 Asn Leu Leu Lys His Leu Gly Ile Leu Ile Ala Ile Arg Ile Ile Ser
 290 295 300
 Cys Thr Asn Gly Ile Tyr Tyr Ser Leu Tyr Lys Glu Tyr Tyr Phe Lys
 305 310 315 320
 Tyr Asp Phe Asp Ile Asp Asn Ile Ser Ser Met Phe Lys Val Phe Phe
 325 330 335
 Leu Lys Asn Lys Pro Glu Arg Met Arg Val Tyr Glu Asn Ile
 340 345 350

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Arg Ile Tyr Ser Leu Ile Asp Ser Gln Thr Leu Met Thr Lys Gly
 1 5 10 15
 Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys Lys Trp Asp
 20 25 30
 Ile Ala Lys Lys Lys Gly Gly Met Arg Thr Ile Tyr His Pro Ser Ser
 35 40 45
 Lys Val Lys Leu Ile Gln Tyr Trp Leu Met Asn Asn Val Phe Ser Lys
 50 55 60
 Leu Pro Met His Asn Ala Ala Tyr Ala Phe Val Lys Asn Arg Ser Ile
 65 70 75 80
 Lys Ser Asn Ala Leu Leu His Ala Glu Ser Lys Asn Lys Tyr Tyr Val
 85 90 95

Lys	Ile	Asp	Leu	Lys	Asp	Phe	Phe	Pro	Ser	Ile	Lys	Phe	Thr	Asp	Phe		
			100					105					110				
Glu	Tyr	Ala	Phe	Thr	Arg	Tyr	Arg	Asp	Arg	Ile	Glu	Phe	Thr	Thr	Glu		
		115					120					125					
Tyr	Asp	Lys	Glu	Leu	Leu	Gln	Leu	Ile	Lys	Thr	Ile	Cys	Phe	Ile	Ser		
	130					135					140						
Asp	Ser	Thr	Leu	Pro	Ile	Gly	Phe	Pro	Thr	Ser	Pro	Leu	Ile	Ala	Asn		
145					150					155					160		
Phe	Val	Ala	Arg	Glu	Leu	Asp	Glu	Lys	Leu	Thr	Gln	Lys	Leu	Asn	Ala		
				165					170					175			
Ile	Asp	Lys	Leu	Asn	Ala	Thr	Tyr	Thr	Arg	Tyr	Ala	Asp	Asp	Ile	Ile		
			180					185					190				
Val	Ser	Thr	Asn	Met	Lys	Gly	Ala	Ser	Lys	Leu	Ile	Leu	Asp	Cys	Phe		
		195					200					205					
Lys	Arg	Thr	Met	Lys	Glu	Ile	Gly	Pro	Asp	Phe	Lys	Ile	Asn	Ile	Lys		
	210					215					220						
Lys	Phe	Lys	Ile	Cys	Ser	Ala	Ser	Gly	Gly	Ser	Ile	Val	Val	Thr	Gly		
225					230					235					240		
Leu	Lys	Val	Cys	His	Asp	Phe	His	Ile	Thr	Leu	His	Arg	Ser	Met	Lys		
				245					250					255			
Asp	Lys	Ile	Arg	Leu	His	Leu	Ser	Leu	Leu	Ser	Lys	Gly	Ile	Leu	Lys		
			260					265					270				
Asp	Glu	Asp	His	Asn	Lys	Leu	Ser	Gly	Tyr	Ile	Ala	Tyr	Ala	Lys	Asp		
		275					280					285					
Ile	Asp	Pro	His	Phe	Tyr	Thr	Lys	Leu	Asn	Arg	Lys	Tyr	Phe	Gln	Glu		
	290					295					300						
Ile	Lys	Trp	Ile	Gln	Asn	Leu	His	Asn	Lys	Val	Glu						
305					310					315							

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 548..1507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

TGGCATCTAT TAAGAAGGTT AGGAAAGAAA ATAAAGTATC AAAAGATATT GGAAATATAT      60
TATACGCAGA GCGTTTCTAT TGCCTTGTAT CTATTTACTG GATAGTGTCA ACTACCGCAC      120
ACTGTGTGAA CTAGCTTTTA AAGCGATAAA GCAAGATGAT GTTTTATCTA AAATTATTGT      180
TAGATCCGTT GTTTCTCGTC TAATAAATGA ACGAAAAATA CTTCAAATGA CTGATGGTTA      240
TCAGGTCACT GCTTTGGGGG CTAGCTATGT TAGGAGCGTC TTTGATAGAA AGACACTTGA      300
CCGATTGCGG CTTGAGATTA TGAATTTTGA AAACCGTAGA AAATCAACAT TTAACTATGA      360
TAAGATTCCG TATGCGCACC CTTAGCGAGA GGTTTATCAT TAAGGTCAAC CTCTGGATGT      420
TGTTTCGGCA TCCTGCATTG AATCTGAGTT ACTGTCTGTT TTCCTTGTTG GAACGGAGAG      480
CATCGCCTGA TGCTCTCCGA GCCAACCAGG AAACCCGTTT TTTCTGACGT AAGGGTGCGC      540
AACTTTC ATG AAA TCC GCT GAA TAT TTG AAC ACT TTT AGA TTG AGA AAT      589
      Met Lys Ser Ala Glu Tyr Leu Asn Thr Phe Arg Leu Arg Asn
          1             5             10

CTC GGC CTA CCT GTC ATG AAC AAT TTG CAT GAC ATG TCT AAG GCG ACT      637
Leu Gly Leu Pro Val Met Asn Asn Leu His Asp Met Ser Lys Ala Thr
   15             20             25             30

CGC ATA TCT GTT GAA ACA CTT CGG TTG TTA ATC TAT ACA GCT GAT TTT      685
Arg Ile Ser Val Thr Leu Arg Leu Ile Tyr Thr Ala Asp Phe
          35             40             45

CGC TAT AGG ATC TAC ACT GTA GAA AAG AAA GGC CCA GAG AAG AGA ATG      733
Arg Tyr Arg Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met
          50             55             60

AGA ACC ATT TAC CAA CCT TCT CGA GAA CTT AAA GCC TTA CAA GGA TGG      781
Arg Thr Ile Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp
          65             70             75

GTT CTA CGT AAC ATT TTA GAT AAA CTG TCG TCA TCT CCT TTT TCT ATT      829
Val Leu Arg Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile
          80             85             90

GGA TTT GAA AAG CAC CAA TCT ATT TTG AAT AAT GCT ACC CCG CAT ATT      877
Gly Phe Glu Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile
          95             100             105             110

GGG GCA AAC TTT ATA CTG AAT ATT GAT TTG GAG GAT TTT TTC CCA AGT      925
Gly Ala Asn Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser
          115             120             125

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TTA ACT GCT AAC AAA GTT TTT GGA GTG TTC CAT TCT CTT GGT TAT AAT Leu Thr Ala Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn 130 135 140	973
CGA CTA ATA TCT TCA GTT TTG ACA AAA ATA TGT TGT TAT AAA AAT CTG Arg Leu Ile Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu 145 150 155	1021
CTA CCA CAA GGT GCT CCA TCA TCA CCT AAA TTA GCT AAT CTA ATA TGT Leu Pro Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys 160 165 170	1069
TCT AAA CTT GAT TAT CGT ATT CAG GGT TAT GCA GGT AGT CGG GGC TTG Ser Lys Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu 175 180 185 190	1117
ATA TAT ACG AGA TAT GCC GAT GAT CTC ACC TTA TCT GCA CAG TCT ATG Ile Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met 195 200 205	1165
AAA AAG GTT GTT AAA GCA CGT GAT TTT TTA TTT TCT ATA ATC CCA AGT Lys Lys Val Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser 210 215 220	1213
GAA GGA TTG GTT ATT AAC TCA AAA AAA ACT TGT ATT AGT GGG CCT CGT Glu Gly Leu Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg 225 230 235	1261
AGT CAG AGG AAA GTT ACA GGT TTA GTT ATT TCA CAA GAG AAA GTT GGG Ser Gln Arg Lys Val Thr Gly Leu Val Ile Ser Gln Glu Lys Val Gly 240 245 250	1309
ATA GGT AGA GAA AAA TAT AAA GAA ATT AGA GCA AAG ATA CAT CAT ATA Ile Gly Arg Glu Lys Tyr Lys Glu Ile Arg Ala Lys Ile His His Ile 255 260 265 270	1357
TTT TGC GGT AAG TCT TCT GAG ATA GAA CAC GTT AGG GGA TGG TTG TCA Phe Cys Gly Lys Ser Ser Glu Ile Glu His Val Arg Gly Trp Leu Ser 275 280 285	1405
TTT ATT TTA AGT GTG GAT TCA AAA AGC CAT AGG AGA TTA ATA ACT TAT Phe Ile Leu Ser Val Asp Ser Lys Ser His Arg Arg Leu Ile Thr Tyr 290 295 300	1453
ATT AGC AAA TTA GAA AAA AAA TAT GGA AAG AAC CCT TTA AAT AAA GCG Ile Ser Lys Leu Glu Lys Lys Tyr Gly Lys Asn Pro Leu Asn Lys Ala 305 310 315	1501
AAG ACC TAATGGTCTT CGTTTAAAA CTAAAGCTCA TAGGTTGAAA AATTGAGCAC Lys Thr 320	1557
TTCTTCGTCC AACCAGTTAT TTAGTTCCTG CAATCGTTTC TGCAG	1602

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

Met Lys Ser Ala Glu Tyr Leu Asn Thr Phe Arg Leu Arg Asn Leu Gly
 1           5           10           15
Leu Pro Val Met Asn Asn Leu His Asp Met Ser Lys Ala Thr Arg Ile
          20           25           30
Ser Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe Arg Tyr
          35           40           45
Arg Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met Arg Thr
          50           55           60
Ile Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp Val Leu
          65           70           75           80
Arg Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile Gly Phe
          85           90           95
Glu Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile Gly Ala
          100          105          110
Asn Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser Leu Thr
          115          120          125
Ala Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn Arg Leu
          130          135          140
Ile Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu Leu Pro
          145          150          155          160
Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys Ser Lys
          165          170          175
Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu Ile Tyr
          180          185          190
Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met Lys Lys
          195          200          205
Val Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser Glu Gly
          210          215          220
Leu Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg Ser Gln
          225          230          235          240
Arg Lys Val Thr Gly Leu Val Ile Ser Gln Glu Lys Val Gly Ile Gly
          245          250          255

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 396..1352
```

TCACCCTGAA	AGACCTGATT	GCTTACCTGG	AAGAGAAGCC	GGAAATGGCG	GAACATCTGG												60
CGGCGGTAA	GGCCTATCGC	GAAGAGTTCG	GCGTTTAAAA	ATATGCGCTG	TGCAGGGTTT												120
TTGCTGTGCG	CAGCGTGATG	CGCTTCAAGA	TATCGTGTTA	ATCTGCTTTC	GCCAGCAGTG												180
GCAATAGCGT	TTCCGGCCTT	TTGTGCCGGG	AGGGTCGGCG	AGTCGCTGAC	TTAACGCCAG												240
TAGTATGTCC	ATATACCCAA	AGTCGCTTCA	TTGTACCTGA	GTACGCTTCG	CGTACGTCGC												300
GCTGACGCGC	TCAGTACAGT	TACGCGCCTT	CGGGATGGTT	TAATGGTATT	GCCGCTGTTG												360
GCGCCTCTTT	TGGCCGCCGT	GATGTGGAGA	GTGGA	ATG	GAT	GCT	ACC	CGG	ACA								413
				Met	Asp	Ala	Thr		Arg	Thr							
				1											5		
ACC	CTT	CTG	GCG	CTC	GAT	TTG	TTC	GGC	TCG	CCG	GGC	TGG	AGC	GCC	GAT		461
Thr	Leu	Leu	Ala	Leu	Asp	Leu	Phe	Gly	Ser	Pro	Gly	Trp	Ser	Ala	Asp		
			10					15					20				
AAA	GAA	ATA	CAG	CGA	CTG	CAT	GCG	CTC	AGT	AAT	CAT	GCC	GGA	CGC	CAT		509
Lys	Glu	Ile	Gln	Arg	Leu	His	Ala	Leu	Ser	Asn	His	Ala	Gly	Arg	His		
		25					30					35					
TAC	CGA	CGC	ATT	ATT	CTT	TCT	AAA	CGC	CAC	GGT	GGT	CAG	CGG	CTG	GTG		557
Tyr	Arg	Arg	Ile	Ile	Leu	Ser	Lys	Arg	His	Gly	Gly	Gln	Arg	Leu	Val		
	40					45					50						

TTA GCC CCT GAT TAC TTG CTC AAA ACC GTA CAG CGC AAC ATT CTT AAG	605
Leu Ala Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys	
55 60 65 70	
AAC GTC CTT TCA CAA TTT CCG CTT TCC CCT TTT GCT ACA GCC TAC CGA	653
Asn Val Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg	
75 80 85	
CCA GGT TGC CCA ATC GTC AGC AAC GCG CAG CCA CAC TGC CAA CAG CCG	701
Pro Gly Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro	
90 95 100	
CAG ATC CTG AAA CTC GAT ATC GAA AAC TTT TTC GAT AGC ATT AGC TGG	749
Gln Ile Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp	
105 110 115	
TTA CAG GTC TGG CGT GTG TTT CGC CAG GCC CAG TTG CCA CGT AAT GTG	797
Leu Gln Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val	
120 125 130	
GTA ACC ATG CTG ACC TGG ATT TGT TGT TAT AAC GAC GCG TTA CCG CAG	845
Val Thr Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln	
135 140 145 150	
GGG GCA CCA ACT TCG CCA GCC ATT TCC AAT CTT GTG ATG CGC CGT TTT	893
Gly Ala Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe	
155 160 165	
GAT GAA CGC ATA GGG GAA TGG TGT CAG GCT CGG GGA ATT ACC TAC ACC	941
Asp Glu Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr	
170 175 180	
CGC TAC TGC GAT GAC ATG ACC TTT TCA GGT CAC TTC AAT GCC CGC CAG	989
Arg Tyr Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln	
185 190 195	
GTT AAA AAT AAA GTG TGC GGA TTG TTA GCG GAG CTG GGC CTG AGC CTC	1037
Val Lys Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu	
200 205 210	
AAT AAA CGC AAA GGC TGC CTG ATA GCT GCC TGT AAG CGC CAG CAA GTA	1085
Asn Lys Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val	
215 220 225 230	
ACC GGG ATT GTT GTT AAT CAC AAG CCA CAG CTT GCC CGT GAA GCG CGC	1133
Thr Gly Ile Val Val Asn His Lys Pro Gln Leu Ala Arg Glu Ala Arg	
235 240 245	
CGG GCG CTG CGT CAG GAG GTG CAT TTG TGC CAA AAA TAT GGC GTT ATT	1181
Arg Ala Leu Arg Gln Glu Val His Leu Cys Gln Lys Tyr Gly Val Ile	
250 255 260	
TCG CAT CTT AGT CAT CGT GGT GAA CTT GAT CCT TCT GGC GAT CTC CAC	1229
Ser His Leu Ser His Arg Gly Glu Leu Asp Pro Ser Gly Asp Leu His	
265 270 275	

GCA CAG GCA ACG GCG TAT CTT TAT GCT TTG CAG GGA AGA ATA AAC TGG	1277
Ala Gln Ala Thr Ala Tyr Leu Tyr Ala Leu Gln Gly Arg Ile Asn Trp	
280 285 290	
TTA TTG CAA ATC AAC CCT GAG GAT GAG GCC TTT CAA CAG GCG AGA GAG	1325
Leu Leu Gln Ile Asn Pro Glu Asp Glu Ala Phe Gln Gln Ala Arg Glu	
295 300 305 310	
AGT GTA AAG CGA ATG CTG GTT GCA TGG TAAGAAAAGC GTCAGGCAGA	1372
Ser Val Lys Arg Met Leu Val Ala Trp	
315	
CGTTTCTGCC TGACCGTTTA GGGGAGAATT ACTGCAACTG CGCGGCAATT AGCGGCCAGC	1432
GGGCGTCAAA ATCATCCGTC GGGCGGTATT TAAACTCGCT GCGGACAAAA CGTGACAGCA	1492
TACCTTCACA GAAGGCCAGG ATCTGGCTTG CCAGCAGGGT TTCATCGG	1540

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Asp Ala Thr Arg Thr Thr Leu Leu Ala Leu Asp Leu Phe Gly Ser	
1 5 10 15	
Pro Gly Trp Ser Ala Asp Lys Glu Ile Gln Arg Leu His Ala Leu Ser	
20 25 30	
Asn His Ala Gly Arg His Tyr Arg Arg Ile Ile Leu Ser Lys Arg His	
35 40 45	
Gly Gly Gln Arg Leu Val Leu Ala Pro Asp Tyr Leu Leu Lys Thr Val	
50 55 60	
Gln Arg Asn Ile Leu Lys Asn Val Leu Ser Gln Phe Pro Leu Ser Pro	
65 70 75 80	
Phe Ala Thr Ala Tyr Arg Pro Gly Cys Pro Ile Val Ser Asn Ala Gln	
85 90 95	
Pro His Cys Gln Gln Pro Gln Ile Leu Lys Leu Asp Ile Glu Asn Phe	
100 105 110	
Phe Asp Ser Ile Ser Trp Leu Gln Val Trp Arg Val Phe Arg Gln Ala	
115 120 125	
Gln Leu Pro Arg Asn Val Val Thr Met Leu Thr Trp Ile Cys Cys Tyr	
130 135 140	

Asn	Asp	Ala	Leu	Pro	Gln	Gly	Ala	Pro	Thr	Ser	Pro	Ala	Ile	Ser	Asn
145					150					155					160
Leu	Val	Met	Arg	Arg	Phe	Asp	Glu	Arg	Ile	Gly	Glu	Trp	Cys	Gln	Ala
				165					170					175	
Arg	Gly	Ile	Thr	Tyr	Thr	Arg	Tyr	Cys	Asp	Asp	Met	Thr	Phe	Ser	Gly
			180					185					190		
His	Phe	Asn	Ala	Arg	Gln	Val	Lys	Asn	Lys	Val	Cys	Gly	Leu	Leu	Ala
		195					200					205			
Glu	Leu	Gly	Leu	Ser	Leu	Asn	Lys	Arg	Lys	Gly	Cys	Leu	Ile	Ala	Ala
	210					215					220				
Cys	Lys	Arg	Gln	Gln	Val	Thr	Gly	Ile	Val	Val	Asn	His	Lys	Pro	Gln
225					230					235					240
Leu	Ala	Arg	Glu	Ala	Arg	Arg	Ala	Leu	Arg	Gln	Glu	Val	His	Leu	Cys
				245					250					255	
Gln	Lys	Tyr	Gly	Val	Ile	Ser	His	Leu	Ser	His	Arg	Gly	Glu	Leu	Asp
			260					265					270		
Pro	Ser	Gly	Asp	Leu	His	Ala	Gln	Ala	Thr	Ala	Tyr	Leu	Tyr	Ala	Leu
		275					280					285			
Gln	Gly	Arg	Ile	Asn	Trp	Leu	Leu	Gln	Ile	Asn	Pro	Glu	Asp	Glu	Ala
	290					295					300				
Phe	Gln	Gln	Ala	Arg	Glu	Ser	Val	Lys	Arg	Met	Leu	Val	Ala	Trp	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Tyr Xaa Asp Asp
1

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Xaa Val Thr Gly
1

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..14
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:

 (A) NAME/KEY: misc_feature
 (B) LOCATION: 16..17
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 20
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 27..28
 (D) OTHER INFORMATION: /product= variable amino acid residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 33..34
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 36..38
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 48..49
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 50..51
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 52
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 53
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 56
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 57
 (D) OTHER INFORMATION: /product= variable small, polar amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 58..65
 (D) OTHER INFORMATION: /product= variable amino acid residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 66
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 67
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /product= Phe or Tyr.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 72..73
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 78
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 82..83
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 84..85
 (D) OTHER INFORMATION: /product= variable amino acid
 residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 86
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 88..89
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 90..92
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 94
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 96
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 104
 (D) OTHER INFORMATION: /product= variable small, polar
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 107
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /product= variable small, polar amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 111..112
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 113..122
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 123
 (D) OTHER INFORMATION: /product= Ser or Thr.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 124..125
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 126
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 127..144
 (D) OTHER INFORMATION: /product= variable amino acid residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 145
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 146
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 147..151
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 152
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 162
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 163
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 164
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 166..167
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 168..169
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 170
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 173
 (D) OTHER INFORMATION: /product= variable small, polar
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 176..177
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 178
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 179
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 180..182
 (D) OTHER INFORMATION: /product= variable amino acid
 residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 183..184
 (D) OTHER INFORMATION: /product= variable small, polar
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 185
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 187
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 193
 (D) OTHER INFORMATION: /product= Ala or Cys.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 196
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 198
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 200
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 201..202
 (D) OTHER INFORMATION: /product= variable small, polar amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 203..205
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 206..219
 (D) OTHER INFORMATION: /product= variable amino acid residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 220
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 221
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 222..224
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 225
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 226
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 227
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 228..229
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 230
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 231
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 232
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 234
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 235
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 236
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 237..239
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 242
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 243
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 244..245
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 246
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid sequence.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 247..248
 (D) OTHER INFORMATION: /product= variable amino acid
residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 249
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 250..251
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

```

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION: 258
      (D) OTHER INFORMATION: /product= variable amino acid
residue.

```

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	
1				5				10					15		
Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Gly	Gly	Xaa	Xaa	Xaa	Arg	Thr	Xaa
			20					25					30		
Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Leu	Lys	Xaa	Xaa	Gln	Arg	Xaa	Xaa	Leu	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55					60				
Xaa	Xaa	Xaa	Ala	Xaa	Gly	Xaa	Xaa	Xaa	Gly	Xaa	Ser	Ile	Xaa	Xaa	Asn
65					70				75						80
Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Asp	Xaa
				85				90						95	
Lys	Asp	Phe	Phe	Pro	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Gly	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		115					120					125			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		130					135					140			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Pro	Gln	Gly	Ala	Pro	Thr	Ser
145					150					155					160
Pro	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Asp	Xaa	Arg	Leu	Xaa
				165						170				175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Thr	Tyr	Thr	Arg	Tyr
			180					185					190		
Xaa	Asp	Asp	Xaa	Thr	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		195					200					205			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		210				215					220				

```

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
225                               230                               235       240

Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Val Thr Gly
                               245                               250       255

Leu Xaa Val

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7..9
- (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 10..11
 (D) OTHER INFORMATION: /product= variable amino acid
residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 16..17
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 19..21
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 22
 (D) OTHER INFORMATION: /product= Val or Leu.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 24..25
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 27..28
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 30..32
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 33
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 34
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 35
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 36..40
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 41..48
 (D) OTHER INFORMATION: /product= variable amino acid
residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 49..53
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 54
 (D) OTHER INFORMATION: /product= Phe or Tyr.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 55..59
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 61..63
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 65..66
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 67..68
 (D) OTHER INFORMATION: /product= variable amino acid
 residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 69..73
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 74..75
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /product= variable hydrophobic
 amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 80..81
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 86
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 87
 (D) OTHER INFORMATION: /product= variable small, polar
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 88
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 89..90
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /product= Val or Phe.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 92..93
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 94..95
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 96..107
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 108
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 110..127
 (D) OTHER INFORMATION: /product= variable amino acid
residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 128..138
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 140
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 142
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 145
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 146
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 147
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 149..150
 (D) OTHER INFORMATION: /product= variable hydrophobic
amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 151..153
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 154
 (D) OTHER INFORMATION: /product= Met, Phe or Leu.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 156
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 157
 (D) OTHER INFORMATION: /product= Lys or Arg.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 158
 (D) OTHER INFORMATION: /product= Ile or Leu.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 159..162
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 163..165
 (D) OTHER INFORMATION: /product= variable amino acid
residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 166..171
 (D) OTHER INFORMATION: /product= variable amino acid
residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 173
 (D) OTHER INFORMATION: /product= Ser or Thr.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 176
 (D) OTHER INFORMATION: /product= Ala or Cys.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 179
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 180
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 181
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 183
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 184
 (D) OTHER INFORMATION: /product= variable small, polar amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 185..188
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 189..202
 (D) OTHER INFORMATION: /product= variable amino acid residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 203
 (D) OTHER INFORMATION: /product= variable amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 204
 (D) OTHER INFORMATION: /product= variable hydrophobic amino acid residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 205..222
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 224..229
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 230..231
 (D) OTHER INFORMATION: /product= variable amino acid
 residue or not present.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 232..236
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 240
 (D) OTHER INFORMATION: /product= Ile, Leu or Val.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 241
 (D) OTHER INFORMATION: /product= variable amino acid
 residue.

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 242
 (D) OTHER INFORMATION: /product= Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	1	5	10	15
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Ala	50	55	60	

